

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:38:30 : Search time 95 Seconds
(without alignments)
1178.804 Million cell updates/sec

Perfect score: 63

Sequence: 1 gagctttctccaggatgg... gctatatttagggggcgaa 63

Scoring table: IDENTITY_NUC

Gapext 1.0 , Gapext 1.0

Searched: 1303057 seqs,

888780828 residues

Total number of hits satisfying chosen parameters:

2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$
Maximum Match 100\$
Listing First 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/1_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/H_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/PP_COMB.seq: *
7: /cgn2_6/ptodata/1/ina/RB_COMB.seq: *
8: /cgn2_6/ptodata/1/ina/RB_COMB.seq: *
9: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.6	53.3	127	3 US-09-635-132-16	Sequence 16, Appl
2	33.6	53.3	129	2 US-09-189-256A-25	Sequence 25, Appl
3	33.6	53.3	129	3 US-09-193-853-25	Sequence 19, Appl
4	33.6	53.3	140	2 US-08-189-256A-19	Sequence 19, Appl
5	33.6	53.3	140	3 US-09-193-853-19	Sequence 1, Appl
6	33.6	53.3	150	2 US-08-189-256A-1	Sequence 1, Appl
7	33.6	53.3	150	3 US-09-193-853-1	Sequence 1, Appl
8	33.6	53.3	161	2 US-08-189-256A-18	Sequence 18, Appl
9	33.6	53.3	161	3 US-09-193-853-18	Sequence 18, Appl
10	33.6	53.3	164	2 US-08-189-256A-26	Sequence 26, Appl
11	33.6	53.3	164	3 US-09-193-853-26	Sequence 26, Appl
12	33.6	53.3	165	2 US-08-189-256A-4	Sequence 4, Appl
13	33.6	53.3	165	3 US-09-193-853-4	Sequence 4, Appl
14	33.6	53.3	168	2 US-08-189-256A-2	Sequence 2, Appl
15	33.6	53.3	168	3 US-09-193-853-2	Sequence 2, Appl
16	33.6	53.3	168	3 US-09-351-123-5	Sequence 5, Appl
17	33.6	53.3	184	3 US-09-283-419-3	Sequence 5, Appl
18	33.6	53.3	201	3 US-09-011-336-58	Sequence 58, Appl
19	33.6	53.3	202	3 US-09-843-324A-1	Sequence 1, Appl
20	33.6	53.3	244	3 US-09-351-123-6	Sequence 6, Appl
21	33.6	53.3	244	3 US-09-843-324A-2	Sequence 6, Appl
22	33.6	53.3	258	2 US-08-189-256A-24	Sequence 24, Appl
23	33.6	53.3	258	3 US-09-193-853-24	Sequence 24, Appl
24	33.6	53.3	300	3 US-09-202-316-4	Sequence 1, Appl

ALIGNMENTS

Sequence 7, Appli	33.6	53.3	300	3 US-09-202-316-7
Sequence 10, Appli	33.6	53.3	134	3 US-09-193-853-10
Sequence 11, Appli	33.6	53.3	143	3 US-09-142-114-B-6
Sequence 12, Appli	33.6	53.3	1208	3 US-09-193-853-28
Sequence 13, Appli	33.6	53.3	1416	2 US-08-189-256A-27
Sequence 14, Appli	33.6	53.3	1416	2 US-09-193-853-27
Sequence 15, Appli	33.6	53.3	1417	3 US-09-142-114-B-7
Sequence 16, Appli	33.6	53.3	2962	2 US-08-189-256A-3
Sequence 17, Appli	33.6	53.3	2962	2 US-09-193-853-3
Sequence 18, Appli	33.6	53.3	677	3 US-09-936-388-63
Sequence 19, Appli	30.4	48.3	369	3 US-09-265-319-10
Sequence 20, Appli	39.4	48.3	193	3 US-09-142-114-B-5
Sequence 21, Appli	30.4	48.3	7455	3 US-09-220-557-19
Sequence 22, Appli	40	48.3	7455	3 US-10-219-227-19
Sequence 23, Appli	27	42.9	139	2 US-08-217-160-13
Sequence 24, Appli	27	42.9	146	2 US-08-217-360-17
Sequence 25, Appli	27	42.9	171	2 US-08-217-C-32
Sequence 26, Appli	26.6	42.2	133	3 US-09-945-283-C-32
Sequence 27, Appli	25.6	40.6	185	3 US-09-283-419-1

RESULT 1	US-09-635-132-16	Sequence 16, Application US/09635132
		; Patent No. 6620601
		; GENERAL INFORMATION:
		; APPLICANT: NAKASHITA, HIRO
		; APPLICANT: YAMAGUCHI, ISAMU
		; APPLICANT: YOSHIOKA, KEIKO
		; TITLE OF INVENTION: METHODS FOR TRANSFORMED
		; TITLE OF INVENTION: PLANTS AND PROCESSES FOR PREPARATION OF POLYESTERS
		; FILE REFERENCE: 081356/0148
		; CURRENT APPLICATION NUMBER: US/09/635,132
		; CURRENT FILING DATE: 2000-08-09
		; PRIOR APPLICATION NUMBER: JP 11-225832
		; PRIOR FILING DATE: 1999-08-09
		; PRIOR APPLICATION NUMBER: JP 11-225839
		; PRIOR FILING DATE: 1999-08-09
		; NUMBER OF SEQ ID NOS: 18
		; SOFTWARE: PatentIn Ver. 2.1
		; SEQ ID NO 16
		; LENGTH: 127
		; TYPE: DNA
		; ORGANISM: Nicotiana tabacum
		; US-09-635-132-16
		; Query Match
		; Best Local Similarity 53.3%; Score 33.6%; DB 3; Length 127;
		; Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy	16	GTCGGATTGAGCTAGGGGGCTCTAGGGCTATTAGGGGGCGGAA 63
Db	53	GTCGGATTGAGCTAGGGGGCTCTAGGGCTATTAGGGGGCGGAA 100

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.6	53.3	127	3 US-09-635-132-16	Sequence 16, Appl
2	33.6	53.3	129	2 US-08-189-256A-25	Sequence 25, Appl
3	33.6	53.3	129	3 US-09-193-853-25	Sequence 19, Appl
4	33.6	53.3	140	2 US-08-189-256A-19	Sequence 19, Appl
5	33.6	53.3	140	3 US-09-193-853-19	Sequence 1, Appl
6	33.6	53.3	150	2 US-08-189-256A-1	Sequence 1, Appl
7	33.6	53.3	150	3 US-09-193-853-1	Sequence 1, Appl
8	33.6	53.3	161	2 US-08-189-256A-18	Sequence 18, Appl
9	33.6	53.3	161	3 US-09-193-853-18	Sequence 18, Appl
10	33.6	53.3	164	2 US-08-189-256A-26	Sequence 26, Appl
11	33.6	53.3	164	3 US-09-193-853-26	Sequence 26, Appl
12	33.6	53.3	165	2 US-08-189-256A-4	Sequence 4, Appl
13	33.6	53.3	165	3 US-09-193-853-4	Sequence 4, Appl
14	33.6	53.3	168	2 US-08-189-256A-2	Sequence 2, Appl
15	33.6	53.3	168	3 US-09-193-853-2	Sequence 2, Appl
16	33.6	53.3	168	3 US-09-351-123-5	Sequence 5, Appl
17	33.6	53.3	184	3 US-09-283-419-3	Sequence 5, Appl
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22	33.6	53.3	258	2 US-08-189-256A-24	Sequence 24, Appl
23	33.6	53.3	258	3 US-09-193-853-24	Sequence 24, Appl
24	33.6	53.3	300	3 US-09-202-316-4	Sequence 4, Appl

TITLE OF INVENTION: DNA Constructs and Methods for Stably Transforming Plastids of Multicellular Plants and Expressing Recombinant Proteins Therein

TITLE OF INVENTION: 47

NUMBER OF SEQUENCES: 47

CCORRESPONDENCE ADDRESS:

ADDRESSEE: Darn, Dorfman, Herrell and Skillman

STREET: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

 MEDIUM TYPE: Floppy disk

 COMPUTER: IBM PC compatible

 OPERATING SYSTEM: PC-DOS/MS-DOS

 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/189,256A

FILING DATE: 31-JAN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/111,398

FILING DATE: 25-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/518,763

FILING DATE: 01-MAY-1990

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 563-4100

TELEFAX: (215) 563-1044

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 129 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLCULE TYPE: DNA (Genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

SUL3T 3
 - 09-193-853-25
 Sequence Application US/09193853
 Patent No. 6388168
 GENERAL INFORMATION:
 APPLICANT: Maliga, Pal
 APPLICANT: Svab, Zora
 APPLICANT: Staub, Jeffrey
 APPLICANT: Zoubenko, Oleg V.
 APPLICANT: Allison, Lori A.
 APPLICANT: Cramer, Helaine
 APPLICANT: Kaneyuki, Ivan
 TITLE OF INVENTION: DNA Constructs and Methods for Stably Transforming Plastids of Multicellular Plants and Title of Invention: Expressing Recombinant Proteins Therein
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Darn, Dorfman, Herrrell and Skillman
 STREET: 1601 Market Street Suite 720
 CITY: Philadelphia

COUNTRY: USA
 ZIP: 19103-2107
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentus Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/193,853
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/189,256
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,763
 FILING DATE: 01-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Janet E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 TELEFAX: (215) 563-4044
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 129 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-09-193-853-25

Query Match 53.3%; Score 33.6; DB 3; 1
 Best Local Similarity 81.2%; Pred. No. 0.0011; 1;
 Matches 39; Conservative 0; Mismatches 9;
 Qy 16 GTGGGATGACGTGAGGGGTCTTAGGGCTATATTAGGG
 Db 46 GTGGGATGACGTGAGGGGTCTAGGGCTATATTCTGGCT

RESULT 4
US-08-189-256A-19
Sequence 19, Application US/08189256A
Patent No. 5877402
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Svab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenko, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carrer, Helaine
APPLICANT: Kanevski, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably Transforming Plastids of Multicellular Plants and Expressing Recombinant Proteins Therein
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILED DATE: 08/01/1996
PUBLICATION DATE: 03/10/1997
EXPIRATION DATE: 08/01/2016

FILING DATE: 31-JAN-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/111,398
 FILING DATE: 25-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,763
 FILING DATE: 01-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Janet E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 TELEFAX: (215) 563-4044
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 140 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 TELEFAX: (215) 563-4100
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 140 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-189-256A-19

Query Match 53.3%: Score 33.6; DB 2; Length 140;
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 Matches 39; Conservative 0; Mismatches 9; Indels 0;
 Gaps 0;

RESULT 5
 US-09-191-853-19
 Sequence 19, Application US/09193853
 GENERAL INFORMATION:
 PATENT NO. 6388168
 APPLICANT: Maligna, Pal
 APPLICANT: Svab, Zora
 APPLICANT: Staub, Jeffrey V.
 APPLICANT: Zoubenko, Oleg V.
 APPLICANT: Allison, Lori A.
 APPLICANT: Carrier, Helaine
 APPLICANT: Kanevski, Ivan
 TITLE OF INVENTION: DNA Constructs and Methods for Stably
 Transforming Plastids of Multicellular Plants and
 Expressing Recombinant Proteins Therein
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dann, Dorfman, Herrell and Skillman
 STREET: 1601 Market Street Suite 720
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-2307
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/189,256A
 FILING DATE: 31-JAN-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/111,398
 FILING DATE: 25-AUG-1993
 PRIORITY APPLICATION NUMBER: US 07/518,763
 FILING DATE: 01-MAY-1990
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/09/193,853
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/189,256
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,763
 FILING DATE: 01-MAY-1990
 ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 TELEFAX: (215) 563-4044
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 150 base pairs
 TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: not relevant
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-09-189-256A-1

Query Match 53.3%; Score 33.6; DB 2; Length 150;
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

RESULT 7
 Query 16 GTGGGATTGACGTGAGGGCTAGGCTATATTAGGGAGCGAA 63
 Db 41 GTGGGATTGACGTGAGGGCTAGGCTATATTCTGGAGCGAA 88

RESULT 8
 Query 16 GTGGGATTGACGTGAGGGCTAGGCTATATTAGGGAGCGAA 63
 Db 41 GTGGGATTGACGTGAGGGCTAGGCTATATTCTGGAGCGAA 88

US-09-193-853-1
 Sequence 1, Application US/09193853
 Patent No. 6388168
 GENERAL INFORMATION:
 APPLICANT: Maliga, Pal
 APPLICANT: Svab, Zora
 APPLICANT: Staub, Jeffrey V.
 APPLICANT: Zoubenko, Oleg V.
 APPLICANT: Allison, Lori A.
 APPLICANT: Carter, Helaine
 APPLICANT: Kanavski, Ivan
 TITLE OF INVENTION: DNA Constructs and Methods for Stably Transforming Plasmids of Multicellular Plants and Expressing Recombinant Proteins Therein
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dann, Dorfman, Herrell and Skillman
 STREET: 1601 Market Street Suite 720
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-2307
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/193,853
 FILING DATE: 08/09/1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/189,256A
 FILING DATE: 31-JAN-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/111,398
 FILING DATE: 25-AUG-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,763
 FILING DATE: 01-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Janet E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 TELEFAX: (215) 563-4044
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 161 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-09-189-256A-18

Query Match 53.3%; Score 33.6; DB 2; Length 161;
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

RESULT 9
 Query Match 53.3%; Score 33.6; DB 3; Length 150;
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 US-09-193-853-18

Sequence 18, Application US/09193853
 Patent No. 6388168
 GENERAL INFORMATION:
 APPLICANT: Maliga, Pal
 APPLICANT: Svab, Zora
 APPLICANT: Staub, Jeffrey
 APPLICANT: Zoubenko, Oleg V.
 APPLICANT: Allison, Lori A.
 APPLICANT: Carrer, Helaine
 APPLICANT: Kanevski, Ivan
 TITLE OF INVENTION: DNA Constructs and Methods for Stably Expressing Plastics of Multicellular Plants and Recombinant Proteins Therein
 TITLE OF INVENTION: Expressing Recombinant Proteins Therein
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dann, Dorman, Herrell and Skillman
 STREET: 1601 Market Street Suite 720
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103-2307
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/193,853
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/189,256
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,763
 FILING DATE: 01-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Janet E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 TELEFAX: (215) 563-4044
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 161 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-09-193-853-18

Query Match 53.3%; Score 33.6; DB 3; Length 161;
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0

Qy 16 GTCGGATTGACGTGAGGGGGCTCCCTAGGCCTATTAGACGGAGCGAA 63
 Db 63 GTCGGATTGACGTGAGGGGGCTCCCTAGGCCTATTAGACGGAGCGAA 110

RESULT 10
 US-08-189-256A-26
 ; Sequence 26, Application US/08189256A
 ; Patent No. 5877402
 GENERAL INFORMATION:
 APPLICANT: Maliga, Pal
 APPLICANT: Svab, Zora
 APPLICANT: Staub, Jeffrey
 APPLICANT: Zoubenko, Oleg V.
 APPLICANT: Allison, Lori A.
 APPLICANT: Carrer, Helaine

```

APPLICANT: Kanevsky, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,256A
FILING DATE: 31-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,398
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/518,763
FILING DATE: 01-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-189-256A-26

RESULT 11
US-09-193-853-26
Sequence 26, Application US/09193853
Patent No. 6388168
GENERAL INFORMATION:
APPLICANT: Maliga, Pal
APPLICANT: Srab, Zora
APPLICANT: Staub, Jeffrey
APPLICANT: Zoubenkov, Oleg V.
APPLICANT: Allison, Lori A.
APPLICANT: Carter, Helaine
APPLICANT: Kanevsky, Ivan
TITLE OF INVENTION: DNA Constructs and Methods for Stably
TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and
TITLE OF INVENTION: Expressing Recombinant Proteins Therein
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307

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APPLICATION NUMBER: US/08/189,256A
 FILING DATE: 31-JAN-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: APPLICATION NUMBER: US/09/193,853
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/189,256
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/518,763
 FILING DATE: 01-MAY-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Janet E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 TELEFAX: (215) 563-4044
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 164 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-189-256A-4

Query Match 53.3%; Score 33.6; DB 3; Length 164;
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 Matches 39; Conservative 0; Mismatches 9; Indels 0;
 Gaps 0;

RESULT 13
 US-09-193-853-4
 ; Sequence 4, Application US/09193853
 ; Patent No. 6388168
 ; GENERAL INFORMATION:
 ; COMPUTER: DNA Constructs and Methods for Stably
 ; TITLE OF INVENTION: DNA Constructing Plastids of Multicellular Plants and
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/193,853
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/189,256
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/518,763
 ; FILING DATE: 01-MAY-1990

Query Match 53.3%; Score 33.6; DB 2; Length 165;
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 Matches 39; Conservative 0; Mismatches 9; Indels 0;
 Gaps 0;

Qy 16 GTGGGATTGACCTGAGGGGCTCCCTAGGCTATATTAGGGAGCGAA 63
 Db 41 GTGGGATTGACCTGAGGGCAGGGATGGTATTCTGGAGCGAA 88

RESULT 12
 US-08-189-256A-4
 ; Sequence 4, Application US/08189256A
 ; Patent No. 5877402
 ; GENERAL INFORMATION:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/189,256
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/189,256
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/518,763
 ; FILING DATE: 01-MAY-1990

Query Match 53.3%; Score 33.6; DB 3; Length 164;
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 Matches 39; Conservative 0; Mismatches 9; Indels 0;
 Gaps 0;

Qy 16 GTGGGATTGACCTGAGGGGCTCCCTAGGCTATATTAGGGAGCGAA 63
 Db 46 GTGGGATTGACCTGAGGGCAGGGATGGTATTCTGGAGCGAA 93

RESULT 12
 US-08-189-256A-4
 ; Sequence 4, Application US/08189256A
 ; Patent No. 5877402
 ; GENERAL INFORMATION:
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/189,256
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/189,256
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/518,763
 ; FILING DATE: 01-MAY-1990

Query Match 53.3%; Score 33.6; DB 3; Length 164;
 Best Local Similarity 81.2%; Pred. No. 0.0012;
 Matches 39; Conservative 0; Mismatches 9; Indels 0;
 Gaps 0;

Qy 16 GTGGGATTGACCTGAGGGGCTCCCTAGGCTATATTAGGGAGCGAA 63
 Db 47 GTGGGATTGACCTGAGGGCAGGGATGGTATTCTGGAGCGAA

ATTORNEY/AGENT INFORMATION:
 NAME: Reed, Janet E.
 REGISTRATION NUMBER: 36,252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 563-4100
 FAX: (215) 563-4044
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 165 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-09-193-853-4

Query Match 53.3% Score 33.6; DB 3; Length 165;
 Best Local Similarity 81.2%; Pred. No. 0.0012; Indels 0; Gaps 0;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

RESULT 14
 US-08-189-256A-2
 ; Sequence 2, Application US/08189256A
 ; Patent No. 5377402
 ; GENERAL INFORMATION:
 ; APPLICANT: Maliga, Pal
 ; APPLICANT: Svab, Zora
 ; APPLICANT: Staub, Jeffrey
 ; APPLICANT: Zoubenko, Oleg V.
 ; APPLICANT: Carrer, Helaine
 ; APPLICANT: Allison, Lori A.
 ; APPLICANT: Kanevski, Ivan
 ; TITLE OF INVENTION: DNA Constructors and Methods for Stably
 ; Transforming Plastids of Multicellular Plants and
 ; Expressing Recombinant Proteins Therein
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
 ; STREET: 1601 Market Street Suite 720
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103-2307
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 31-JAN-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/111,398
 ; FILING DATE: 25-AUG-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/518,763
 ; FILING DATE: 01-MAY-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reed, Janet E.
 ; REGISTRATION NUMBER: 36,252
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 563-4100
 ; FAX: (215) 563-4044
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 168 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 US-09-193-853-2

Query Match 53.3% Score 33.6; DB 3; Length 168;
 Best Local Similarity 81.2%; Pred. No. 0.0012; Indels 0; Gaps 0;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Query Match 53.3% Score 33.6; DB 2; Length 168;
 Best Local Similarity 81.2%; Pred. No. 0.0012; Indels 0; Gaps 0;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 GTGGGATTGACGTGAGGGCTCCAGGTATATTAGGGGCGAA 63
 Db 41 GTGGGATTGACGTGAGGGCGATGGATGGCTATTCGGAGCGAA 88

RESULT 15
 US-09-193-853-2
 ; Sequence 2, Application US/09193853
 ; Patent No. 6388168
 ; GENERAL INFORMATION:
 ; APPLICANT: Maliga, Pal
 ; APPLICANT: Svab, Zora
 ; APPLICANT: Staub, Jeffrey
 ; APPLICANT: Zoubenko, Oleg V.
 ; APPLICANT: Carrer, Helaine
 ; APPLICANT: Allison, Lori A.
 ; APPLICANT: Kanevski, Ivan
 ; TITLE OF INVENTION: DNA Constructors and Methods for Stably
 ; Transforming Plastids of Multicellular Plants and
 ; Expressing Recombinant Proteins Therein
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dann, Dorfman, Herrell and Skillman
 ; STREET: 1601 Market Street Suite 720
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103-2307
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/193,853
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/189,256
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; APPLICATION NUMBER: US 07/518,763
 ; FILING DATE: 01-MAY-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Reed, Janet E.
 ; REGISTRATION NUMBER: 36,252
 ; TELEPHONE: (215) 563-4100
 ; FAX: (215) 563-4044
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 168 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 US-09-193-853-2

Query Match 53.3% Score 33.6; DB 3; Length 168;

Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy 16 GTGGATTCACGTGAGGGCTCCCTAGCTATATTAGGGAGCGAA 63
Db 41 GTGGATTCACGTGAGGGCAAGGATGGCTATATTCTGGAGCGAA 88

Search completed: February 21, 2006, 05:40:12
Job time : 95 secs

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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:41:51 ; Search time 410 Seconds
(without alignments) 326.188 Million cell updates/sec

Title: US-10-737-251-51

Perfect score: 63

Sequence: 1 gagctcttcggatgggg...9ctatattagggaggcggaa 63

Scoring table: IDENTITY_NUC Gapop 10.0 , gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New:
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2: /cgn2_6/podata/1/pubpna/US06_NEW_PUB_seq:
3: /cgn2_6/podata/1/pubpna/US07_NEW_PUB_seq:
4: /cgn2_6/podata/1/pubpna/PCF_NEW_PUB_seq:
5: /cgn2_6/podata/1/pubpna/US05_NEW_PUB_seq:
6: /cgn2_6/podata/1/pubpna/US09_NEW_PUB_seq:
7: /cgn2_6/podata/1/pubpna/US10_NEW_PUB_seq:
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11: /cgn2_6/podata/1/pubpna/US11_NEW_PUB_seq:
12: /cgn2_6/podata/1/pubpna/US11_NEW_PUB_seq:
13: /cgn2_6/podata/1/pubpna/US60_NEW_PUB_seq:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	33.6	53.3	176	7	US-10-527-048-14	Sequence 14, App1
2	33.6	53.3	2569	9	US-11-190-122-3	Sequence 3, App1
3	33.6	53.3	2800	9	US-11-190-122-1	Sequence 1, App1
4	33.6	53.3	3119	9	US-11-190-122-5	Sequence 2, App1
5	33.6	53.3	5834	7	US-10-527-048-15	Sequence 15, App1
6	33.6	53.3	6465	7	US-10-527-048-25	Sequence 25, App1
7	33.6	53.3	6659	7	US-10-527-048-22	Sequence 22, App1
8	33.6	53.3	7549	7	US-10-527-048-24	Sequence 24, App1
9	25.6	40.6	562	6	US-09-925-065A-935299	Sequence 935299,
10	25.6	40.6	562	6	US-09-925-065A-935300	Sequence 935300,
11	25.6	40.6	562	6	US-09-925-065A-935295	Sequence 935295,
12	25.6	40.6	562	6	US-09-925-065A-932906	Sequence 932906,
13	25.6	40.6	624	6	US-09-925-065A-693983	Sequence 693983,
14	25.6	40.6	56054	8	US-10-995-561-13402	Sequence 13402, A
15	24.2	38.4	561	6	US-09-925-065A-753058	Sequence 753058,
16	24.2	38.4	561	6	US-09-925-065A-824463	Sequence 824463,
17	24.2	38.4	594	6	US-09-925-065A-303887	Sequence 303887,
18	24.2	38.4	594	6	US-09-925-065A-303888	Sequence 303888,
19	24.2	38.4	594	6	US-09-925-065A-753057	Sequence 753057,
20	24.2	38.4	615	6	US-09-925-065A-753057	Sequence 753057,

ALIGNMENTS

RESULT 1
US-10-527-048-14
; Sequence 14, Application US/10527048
; Publication No. US20060026704A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology
; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
; FILE REFERENCE: Vector for plastid transformation
; CURRENT APPLICATION NUMBER: US/10-527-048
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 14
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
; OTHER INFORMATION: Fragment coding for the promoter region of the plastid 16S
; OTHER INFORMATION: ribosomal RNA (Prnr), with added restriction sites.
US-10-527-048-14

Query Match 53.3%; Score 33.6; DB 7; Length 176;
Best Local Similarity 81.2%; Prd. No. 0.0028;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 16 GGGGATTGACGTAGGGGGCTCCCTAGGCTATTAGGGGGCGGAA 63
Db 56 GGGGATTGACGTAGGGGGCGGATGGATCTGGAGCGAA 103

RESULT 2
US-11-190-122-3
; Sequence 3, Application US/11190122
; Publication No. US2006001964A1
; GENERAL INFORMATION:
; APPLICANT: Daniell, Henry
; TITLE OF INVENTION: Plasmid Genetic Engineering Via Somatic Embryogenesis
; FILE REFERENCE: CHI-T10C3Z2
; CURRENT APPLICATION NUMBER: US/11/190-122
; CURRENT FILING DATE: 2005-07-25
; PRIOR APPLICATION NUMBER: 60/344,704
; PRIOR FILING DATE: 2001-12-26

; PRIOR APPLICATION NUMBER: 10/500,351
 ; PRIOR FILING DATE: 2004-06-25
 ; PRIOR APPLICATION NUMBER: pct/us2003/021157
 ; PRIOR FILING DATE: 2003-07-03
 ; PRIOR APPLICATION NUMBER: 60/590,848
 ; PRIOR FILING DATE: 2004-07-23
 ; PRIOR APPLICATION NUMBER: 60/590,751
 ; PRIOR FILING DATE: 2004-07-23
 ; PRIOR APPLICATION NUMBER: 10/519,821
 ; PRIOR FILING DATE: 2004-12-30
 ; PRIOR APPLICATION NUMBER: 60/400,816
 ; PRIOR FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: 60/393,651
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: 60/393,428
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: pct/us2002/041503
 ; PRIOR FILING DATE: 2002-12-26
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 3
 ; LENGTH: 2569
 ; TYPE: DNA
 ; ORGANISM: ARTIFICIAL
 ; FEATURE:
 ; OTHER INFORMATION: alpha-6/lnptII expression cassette
 US-11-190-122-3

Query Match 53.3%; Score 13.6; DB 9; Length 2569;
 Best Local Similarity 81.2%; Pred. No. 0.004; 9; Indels 0; Gaps 0;
 Matches 39; Conservative 0; Mismatches 9;

Qy 16 GGGGATGACCTGAGGGGCTCCCTAGGCTATATTAGGGAGCGAA 63
 Db 119 GGGGATGACCTGAGGGCAGGGCAGGGCTATTTCTGGAGCGAA 166

RESULT 3
 US-11-190-122-1
 ; Sequence 1, Application US/11190122
 ; Publication No. US2006031964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Daniel, Henry
 ; TITLE OF INVENTION: Plastid Genetic Engineering Via Somatic Embryogenesis
 ; FILE REFERENCE: CHU-T107C322
 ; CURRENT FILING DATE: 2005-07-25
 ; PRIOR APPLICATION NUMBER: 60/344,704
 ; PRIOR FILING DATE: 2001-12-26
 ; PRIOR APPLICATION NUMBER: 10/500,351
 ; PRIOR FILING DATE: 2004-06-25
 ; PRIOR APPLICATION NUMBER: pct/us2003/021157
 ; PRIOR FILING DATE: 2003-07-03
 ; PRIOR APPLICATION NUMBER: 60/590,848
 ; PRIOR FILING DATE: 2004-07-23
 ; PRIOR APPLICATION NUMBER: 10/519,821
 ; PRIOR FILING DATE: 2004-12-30
 ; PRIOR APPLICATION NUMBER: 60/400,816
 ; PRIOR FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: 60/393,651
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: 60/393,428
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: pct/us2002/041503
 ; NUMBER OF SEQ ID NOS: 21
 ; OTHER INFORMATION: PatentIn version 3.2
 ; SEQ ID NO: 2
 ; LENGTH: 3119
 ; TYPE: DNA
 ; ORGANISM: ARTIFICIAL
 ; FEATURE:
 ; OTHER INFORMATION: gfp/BADH expression cassette
 US-11-190-122-2

Query Match 53.3%; Score 33.6; DB 9; Length 3119;
 Best Local Similarity 81.2%; Pred. No. 0.0041; 9; Indels 0; Gaps 0;
 Matches 39; Conservative 0; Mismatches 9;

Qy 16 GGGGATGACCTGAGGGGCTCCCTAGGCTATATTAGGGAGCGAA 63
 Db 119 GGGGATGACCTGAGGGCAGGGCAGGGCTATTTCTGGAGCGAA 166

RESULT 5
 US-10-327-048-15
 ; Sequence 15, Application US/10527048
 ; Publication No. US2006026704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Center for Genetic Engineering and Biotechnology,
 ; FILE REFERENCE: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
 ; TITLE OF INVENTION: VECTOR FOR PLASTID TRANSFORMATION
 ; CURRENT APPLICATION NUMBER: US/10/527,048
 ; CURRENT FILING DATE: 2005-03-07
 ; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 1
 ; LENGTH: 2800
 ; TYPE: DNA
 ; ORGANISM: ARTIFICIAL

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 5834
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
; OTHER INFORMATION: fragment from the vector pVTPA between the rice atpB and
; OTHER INFORMATION: tobacco rbcL borders.
US-10-527-048-15

Query Match 53.3%; Score 33.6; DB 7; Length 6659;
Best Local Similarity 81.2%; Pred. No. 0.0045; Score 33.6; DB 7; Length 6659;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
; Sequence 24, Application US/10527048
; Publication No. US20060026704A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology.
; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
; FILE REFERENCE: Vector for plastid transformation
; CURRENT APPLICATION NUMBER: US/10/327,048
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
US-10-527-048-24

Query Match 53.3%; Score 33.6; DB 7; Length 5834;
Best Local Similarity 81.2%; Pred. No. 0.0044; Score 33.6; DB 7; Length 5834;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
; Sequence 25, Application US/10527048
; Publication No. US20060026704A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology.
; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
; FILE REFERENCE: Vector for plastid transformation
; CURRENT APPLICATION NUMBER: US/10/327,048
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
US-10-527-048-25

Query Match 53.3%; Score 33.6; DB 7; Length 7549;
Best Local Similarity 81.2%; Pred. No. 0.0045; Score 33.6; DB 7; Length 7549;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
; Sequence 24, Application US/10527048
; Publication No. US20060026704A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology.
; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
; FILE REFERENCE: Vector for plastid transformation
; CURRENT APPLICATION NUMBER: US/10/327,048
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
US-10-527-048-24

Query Match 53.3%; Score 33.6; DB 7; Length 2895;
Best Local Similarity 81.2%; Pred. No. 0.0045; Score 33.6; DB 7; Length 2895;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
; Sequence 27, Application US/10527048
; Publication No. US20060026704A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology.
; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
; FILE REFERENCE: Vector for plastid transformation
; CURRENT APPLICATION NUMBER: US/10/327,048
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
US-10-527-048-24

Query Match 53.3%; Score 33.6; DB 7; Length 7549;
Best Local Similarity 81.2%; Pred. No. 0.0045; Score 33.6; DB 7; Length 7549;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
; Sequence 24, Application US/10527048
; Publication No. US20060026704A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology.
; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
; FILE REFERENCE: Vector for plastid transformation
; CURRENT APPLICATION NUMBER: US/10/327,048
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
US-10-527-048-24

Query Match 53.3%; Score 33.6; DB 7; Length 6465;
Best Local Similarity 81.2%; Pred. No. 0.0044; Score 33.6; DB 7; Length 6465;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
; Sequence 22, Application US/10527048
; Publication No. US20060026704A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology.
; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
; FILE REFERENCE: Vector for plastid transformation
; CURRENT APPLICATION NUMBER: US/10/327,048
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
US-10-527-048-22

Query Match 53.3%; Score 33.6; DB 7; Length 6659;
Best Local Similarity 81.2%; Pred. No. 0.0045; Score 33.6; DB 7; Length 6659;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
; Sequence 24, Application US/10527048
; Publication No. US20060026704A1
; GENERAL INFORMATION:
; APPLICANT: Center for Genetic Engineering and Biotechnology.
; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.
; FILE REFERENCE: Vector for plastid transformation
; CURRENT APPLICATION NUMBER: US/10/327,048
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
US-10-527-048-22

Query Match 40.6%; Score 25.6; DB 6; Length 562;
Best Local Similarity 66.1%; Pred. No. 3.5; Score 25.6; DB 6; Length 562;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
; Sequence 29, Application US/10525065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 1088871.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957/086
; SEQ ID NO 935299
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
; OTHER INFORMATION: fragment from the vector pVTPA-HB-aada between the rice atpB and
; OTHER INFORMATION: tobacco rbcL borders.
US-09-925-065A-935299

Query Match 40.6%; Score 25.6; DB 6; Length 562;
Best Local Similarity 66.1%; Pred. No. 3.5; Score 25.6; DB 6; Length 562;
Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
; Sequence 29, Application US/0925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 1088871.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957/086
; SEQ ID NO 935299
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA
; OTHER INFORMATION: fragment from the vector pVTPA-HB-aada between the rice atpB and
; OTHER INFORMATION: tobacco rbcL borders.
US-10-527-048-22

```

Qy 1 GAGCTCTTCGGTGGGATGACCTGAGGGCTCCCTAGGCTATTAGAGG 56
 Db 102 GAGCCCTTCCTCGGCTAGCTCCGAGCGGCTCCCTCGCTGCGGAGG 157

RESULT 10
 US-09-925-065A-935300
 ; Sequence 935300, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,756
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 935300
 ; LENGTH: 562
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-935300

Query Match Score 40.6%; Best Local Similarity 66.1%; Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCGGTGGGATGACCTGAGGGCTCCCTAGGCTATTAGAGG 56
 Db 102 GAGCCCTTCCTCGGCTAGCTCCGAGCGGCTCCCTCGCTGCGGAGG 157

RESULT 11
 US-09-925-065A-952905
 ; Sequence 952905, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,756
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 952905
 ; LENGTH: 562
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-952905

Query Match Score 40.6%; Best Local Similarity 66.1%; Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCGGTGGGATGACCTGAGGGCTCCCTAGGCTATTAGAGG 56
 Db 102 GAGCCCTTCCTCGGCTAGCTCCGAGCGGCTCCCTCGCTGCGGAGG 157

RESULT 12
 US-09-925-065A-952906
 ; Sequence 952906, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,756
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 952906
 ; LENGTH: 562
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-952906

Query Match Score 40.6%; Best Local Similarity 66.1%; Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCGGTGGGATGACCTGAGGGCTCCCTAGGCTATTAGAGG 56
 Db 102 GAGCCCTTCCTCGGCTAGCTCCGAGCGGCTCCCTCGCTGCGGAGG 157

RESULT 13
 US-09-925-065A-693983
 ; Sequence 693983, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108827.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/261,756
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 693983
 ; LENGTH: 624
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-693983

Query Match Score 40.6%; Best Local Similarity 66.1%; Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

US-09-925-065A-693983

Query Match 40.6%; Score 25.6; DB 6; Length 624;
 Best Local Similarity 66.1%; Pred. No. 3..5;
 Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCCAGTGGATTGACCTGAGGGCTTACAGG 56
 Db 5170 GAGCCCTCTCCGGCTAGCTGGCTCCCTGGCTGGGGAGG 500

Query Match 38.4%; Score 24.2; DB 6; Length 561;
 Best Local Similarity 66.0%; Pred. No. 1..2;
 Matches 35; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCCAGTGGATTGACCTGAGGGCTTACAGG 53
 Db 254 GAGCCCTCTCCGGCTAGCTGGCTCCCTAGCTGGTTG 306

Search completed: February 21, 2006, 06:33:19
 Job time : 411 secs

RESULT 14

US-10-995-561-13402

; Sequence 13402, Application US/10995561

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michelle et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF DETECTION AND USES THEREOF

; TITLE OF INVENTION: FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 13402

; LENGTH: 56054

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(56054)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-995-561-13402

Query Match 40.6%; Score 25.6; DB 8; Length 56054;
 Best Local Similarity 66.1%; Pred. No. 6..2;
 Matches 37; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 GAGCTCTTCCAGTGGATTGACCTGAGGGCTTACAGG 56
 Db 5170 GAGCCCTCTCCGGCTAGCTGGCTCCCTGGCTGGGGAGG 5225

RESULT 15

US-09-925-065A-753058

; Sequence 753058, Application US/09925065A

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 753058

; LENGTH: 561

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-925-065A-753058

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 05:40:29 ; Search time 492 Seconds

(without alignments)
 1058.884 Million cell updates/sec

Title: US-10-737-251-51

Perfect score: 63

Sequence: 1 gagacctctcccaagggtggg.gcttatatttagaggaggcggaa 63

Scoring table: IDENTITY-NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 195517084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Listing First 45 summaries

Database : Published Applications NA Main:*

1: /cgn2_6/prodata/1/pubpna/us09a_pubcomb.seq:*

2: /cgn2_6/prodata/1/pubpna/us08_pubcomb.seq:*

3: /cgn2_6/prodata/1/pubpna/us09b_pubcomb.seq:*

4: /cgn2_6/prodata/1/pubpna/us09b_pubcomb.seq:*

5: /cgn2_6/prodata/1/pubpna/us10a_pubcomb.seq:*

6: /cgn2_6/prodata/1/pubpna/us10b_pubcomb.seq:*

7: /cgn2_6/prodata/1/pubpna/us10c_pubcomb.seq:*

8: /cgn2_6/prodata/1/pubpna/us10d_pubcomb.seq:*

9: /cgn2_6/prodata/1/pubpna/us10e_pubcomb.seq:*

10: /cgn2_6/prodata/1/pubpna/us11_pubcomb.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	63	100.0	63	8	US-10-737-251-51	Sequence 51, Appl
2	38.4	61.0	112	8	US-10-737-251-18	Sequence 18, Appl
3	38.4	61.0	112	8	US-10-737-251-19	Sequence 19, Appl
4	38.4	61.0	112	8	US-10-737-251-23	Sequence 23, Appl
5	36.6	58.1	112	8	US-10-737-251-6	Sequence 10, Appl
6	34.8	55.2	112	8	US-10-737-251-9	Sequence 9, Appl
7	33.6	53.3	112	8	US-10-737-251-3	Sequence 3, Appl
8	33.6	53.3	112	8	US-10-737-251-4	Sequence 4, Appl
9	33.6	53.3	112	8	US-10-737-251-5	Sequence 5, Appl
10	33.6	53.3	112	8	US-10-737-251-6	Sequence 6, Appl
11	33.6	53.3	112	8	US-10-737-251-7	Sequence 7, Appl
12	33.6	53.3	112	8	US-10-737-251-8	Sequence 8, Appl
13	33.6	53.3	112	8	US-10-737-251-27	Sequence 27, Appl
14	33.6	53.3	112	8	US-10-737-251-28	Sequence 28, Appl
15	33.6	53.3	112	8	US-10-737-251-29	Sequence 29, Appl
16	33.6	53.3	112	8	US-10-737-251-30	Sequence 6, Appl
17	33.6	53.3	119	8	US-10-881-813-6	Sequence 1, Appl
18	33.6	53.3	202	3	US-09-843-324A-1	Sequence 1, Appl
19	33.6	53.3	220	3	US-10-945-314-3	Sequence 3, Appl
20	33.6	53.3	233	8	US-10-737-251-38	Sequence 38, Appl
21	33.6	53.3	234	8	US-10-737-251-42	Sequence 42, Appl
22	33.6	53.3	244	3	US-09-843-324A-2	Sequence 2, Appl
23	33.6	53.3	1143	6	US-10-460-716-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
 US-10-737-251-51

; Sequence 51, Application US/10737251

; Publication No. US20040221338A1

; GENERAL INFORMATION:

; APPLICANT: Pal Maliga

; INVENTION: Plastid rRNA Operon PromoterElements for

; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression

; FILE REFERENCE: 1594 RUT 03-US3US

; CURRENT APPLICATION NUMBER: 2003-12-15

; PRIORITY FILING DATE: 2003-12-15

; PRIOR APPLICATION NUMBER: 60/433,302

; PRIORITY FILING DATE: 2002-12-13

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 51

; LENGTH: 63

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: mutant Prtn

RESULT 2
 US-10-737-251-51

; Sequence Match 100.0%; Score 63; DB 8; Length 63;

; Best Local Similarity 100.0%; Prtd. No. 2; 6e-15;

; Mismatches 0; Indels 0; Gaps 0;

; GENERAL INFORMATION:

; APPLICANT: Pal Maliga

; INVENTION: Plastid rRNA Operon PromoterElements for

; TITLE OF INVENTION: Construction of Chimeric Promoters for Transgene Expression

```

FILE REFERENCE: 1594 RUT 03-083US
CURRENT APPLICATION NUMBER: US/10/737,251
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: 60/433,302
PRIOR FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Prrn promoter derivative
US-10-737-251-18

Query Match
Best Local Similarity 61.0% ; Score 38.4 ; DB 8 ; Length 112;
Matches 42 ; Conservative 0 ; Mismatches 6 ; Indels 0 ; Gaps 0 ;
SEQ ID NO 19
LENGTH: 112
FEATURE:
OTHER INFORMATION: Prrn promoter derivative
US-10-737-251-19

Query Match
Best Local Similarity 61.0% ; Score 38.4 ; DB 8 ; Length 112;
Matches 42 ; Conservative 0 ; Mismatches 6 ; Indels 0 ; Gaps 0 ;
RESULT 5
US-10-737-251-10
; Sequence 10, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; INVENTION: Plasmid rRNA Operon PromoterElements for Transgene Expression
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prrn promoter derivative
US-10-737-251-10

Query Match
Best Local Similarity 61.0% ; Score 38.4 ; DB 8 ; Length 112;
Matches 42 ; Conservative 0 ; Mismatches 6 ; Indels 0 ; Gaps 0 ;
RESULT 6
US-10-737-251-9
; Sequence 9, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; INVENTION: Plasmid rRNA Operon PromoterElements for Transgene Expression
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prrn promoter derivative
US-10-737-251-9

Query Match
Best Local Similarity 61.0% ; Score 38.4 ; DB 8 ; Length 112;
Matches 42 ; Conservative 0 ; Mismatches 6 ; Indels 0 ; Gaps 0 ;
RESULT 7
US-10-737-251-8
; Sequence 8, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; INVENTION: Plasmid rRNA Operon PromoterElements for Transgene Expression
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prrn promoter derivative
US-10-737-251-8

Query Match
Best Local Similarity 61.0% ; Score 38.4 ; DB 8 ; Length 112;
Matches 42 ; Conservative 0 ; Mismatches 6 ; Indels 0 ; Gaps 0 ;
RESULT 8
US-10-737-251-7
; Sequence 7, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; INVENTION: Plasmid rRNA Operon PromoterElements for Transgene Expression
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prrn promoter derivative
US-10-737-251-7

Query Match
Best Local Similarity 61.0% ; Score 38.4 ; DB 8 ; Length 112;
Matches 42 ; Conservative 0 ; Mismatches 6 ; Indels 0 ; Gaps 0 ;
RESULT 9
US-10-737-251-6
; Sequence 6, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; INVENTION: Plasmid rRNA Operon PromoterElements for Transgene Expression
; TITLE OF INVENTION: Plasmid rRNA Operon PromoterElements for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737,251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prrn promoter derivative
US-10-737-251-6

```


GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
; Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737-251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prrn promoter derivative
; US-10-737-251-7

Query Match 53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0;
Gaps 0;
Db 28 GTGGGATTCGCTTGTAGGGCTCCCTAGGCTTATTTAGGGAGCGAA 63
Db 28 GTGGGATTCGCTTGTAGGGCTCCCTAGGCTTATTTAGGGAGCGAA 75

RESULT 12
US-10-737-251-8
; Sequence 8, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
; Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737-251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 112
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prrn promoter derivative
; US-10-737-251-8

Query Match 53.3%; Score 33.6; DB 8; Length 112;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 39; Conservative 0; Mismatches 9; Indels 0;
Gaps 0;
Db 16 GTGGGATTCGCTTGTAGGGCTCCCTAGGCTTATTTAGGGAGCGAA 63
Db 28 GTGGGATTCGCTTGTAGGGCTCCCTAGGCTTATTTAGGGAGCGAA 75

RESULT 13
US-10-737-251-27
; Sequence 27, Application US/10737251
; Publication No. US20040221338A1
; GENERAL INFORMATION:
; APPLICANT: Pal Maliga
; APPLICANT: Jon Y. Suzuki
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for
; Construction of Chimeric Promoters for Transgene Expression
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: 1594 RUT 03-083US
; FILE REFERENCE: 1594 RUT 03-083US
; CURRENT APPLICATION NUMBER: US/10/737-251
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: 60/433,302
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 112

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Prrn promoter derivative
US-10-737-251-29

Query Match      53.3%;  Score 33.6;  DB 8;  Length 112;
Best Local Similarity 81.2%;  Pred. No. 0.0019;  Indels 0;
Matches 39;  Conservative 0;  Mismatches 9;  Gaps 0;

Qy          16 GTCGGATTCGCTGAGGGGCTCCTAGCTATTTAGGGGACGAA 63
Db          28 GTCGGATTCGCTGAGGGGCTCCTAGCTATTTAGGGGACGAA 75

```

Search completed: February 21, 2006, 05:48:49
Job time : 493 secs

Query Match	50.8%	Score 32; DB 9; Length 243;	AUTHORS	Bunning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., McAlley, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, A.
Best Local Similarity	79.2%	Pred. No. 1.1;	TITLE	HortResearch Apple EST Project
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;			JOURNAL	Unpublished (2004)
			COMMENT	
Qy	16	GTGGGATTCGACGTGAGGGGGCTCCTAGGCTATATTAGGGAGCGAA 63	SEQUENCING FACILITY	The Horticulture and Food Research Institute of New Zealand Ltd
Db	97	GTGGGATTCGACGTGAGGGGGCTCCTAGGCTATATTAGGGAGCGAA 50	CONTACT	Gleave, A.
			TEL	120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
			FAX	00 64 09 815 4200
			EMAIL	est@hortresearch.co.nz.
RESULT 2			LOCATION/QUALIFIERS	
B2457960	295 bp	DNA linear	FEATURES SOURCE	1. .380
LOCUS	BONDTR2TR BO 1.6_2 KB tot	Brassica oleracea genomic clone BONDTR2,	/organism="Malus x domestica"	
DEFINITION	Genomic survey sequence.		/mol_type="mRNA"	
B2457960	GI: 26737897		/db_xref="taxon:3750"	
GSS			/clone="AAA008805"	
Brassica oleracea			/tissue_type="fruit"	
ORGANISM			/dev_stage="59 days after full bloom, seeds removed"	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.			/clone_lib="(AAA) Royal Gala 59 DAFB fruit, seeds removed"	
Ayels, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Worland, J.R., White, O.R. and Town, C.D.			/note="Vector: PBK-CMV; Library sequenced by Genesis Research & Development"	
1 (bases 1 to 295)				
Genome Res. 15 (4), 487-495 (2005)				
15805490				
Contact: Chris Town				
TIGR				
9712 Medical Center Drive, Rockville, MD 20850, USA.				
Tel: 301-838-3523			QUERY MATCH	Score 32; DB 7; Length 380;
Fax: 301-838-0208			BEST LOCAL SIMILARITY	79.2%; Pred. No. 1.1;
Email: cdtown@igr.org			MISMATCHES	0; Mismatches 10; Indels 0; Gaps
DNA is from a doubled haploid provided by Tom Osborn.				
Seq primer: TR				
Class: sheared ends.				
FEATURES SOURCE	1. .295			
/organism="Brassica oleracea"				
/mol_type="genomic DNA"				
/strain="T01000DH3"				
/db_xref="taxon:3712"				
/clone="BONDTR2"				
/clone_lib="BO 1.6_2 KB tot"				
/note="Vector: PHOS1; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into PHOS1 using BstXI linkers"				
ORIGIN				
Query Match	50.8%	Score 32; DB 9; Length 295;		
Best Local Similarity	79.2%	Pred. No. 1.1;		
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;				
Qy	16	GTGGGATTCGACGTGAGGGGGCTCCTAGGCTATATTAGGGAGCGAA 63		
Db	199	GTGGGATTCGACGTGAGGGGGCTCCTAGGCTATATTAGGGAGCGAA 246		
RESULT 3				
CN859023	380 bp	mRNA linear	FEATURES SOURCE	1. .395
LOCUS	00072AAA008805HT (AAAA) Royal Gala 59 DAFB fruit, seeds removed		/organism="Brassica oleracea"	
DEFINITION	Malus x domestica cDNA clone AAA008805, mRNA sequence.		/mol_type="genomic DNA"	
ACCESSION	CN859023		/str="BONDDB3"	
KEYWORDS	CN859023.1 GI: 48114953		/db_xref="taxon:3712"	
ORGANISM	Malus x domestica		/clone="BO 2_3 KB"	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.			/note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"	
1 (bases 1 to 380)				
REFERENCE				

ORIGIN	Query Match	Score 32; DB 9; Length 395;	Best Local Similarity 79.2%; Pred. No. 1.1;	Matches 38; Conservative 0; Mismatches 0;	Indels 10; Gaps 0;	FEATURES	Source	AUTHORS	Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.	
	DEFINITION	domestica cDNA clone AFBC0023961T (AFBC) Royal Gala pre-opened floral bud Malus x domestica	COMMENT	Unpublished (2004)	COMMENT	COMMENT	COMMENT	TITLE	HortResearch Apple EST Project	
Qy	16	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 63	ACCESSION	CN930271	EST.	ORGANISM	Malus x domestica	ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.	
Db	92	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 139	VERSION	CN930271.1	GI:48403084	REFERENCE	1 (bases 1 to 415)	REFERENCE	Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.	
RESULT 5	LOCUS	CN930271	415 bp	mRNA	linear	EST 07-JUN-2004	DEFINITION	Unpublished (2004)	COMMENT	Unpublished (2004)
CN930271	DEFINITION	domestica cDNA clone AFBC0023961T (AFBC) Royal Gala pre-opened floral bud Malus x domestica	COMMENT	Unpublished (2004)	COMMENT	COMMENT	COMMENT	COMMENT	Unpublished (2004)	
Qy	16	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 63	ACCESSION	CN930271	EST.	ORGANISM	Malus x domestica	ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.	
Db	287	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 334	VERSION	CN930271.1	GI:48403084	REFERENCE	1 (bases 1 to 415)	REFERENCE	Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.	
RESULT 5	LOCUS	CN930271	415 bp	mRNA	linear	EST 07-JUN-2004	DEFINITION	domestica cDNA clone AFBC0023961T (AFBC) Royal Gala pre-opened floral bud Malus x domestica	COMMENT	Unpublished (2004)
CN930271	DEFINITION	domestica cDNA clone AFBC0023961T (AFBC) Royal Gala pre-opened floral bud Malus x domestica	COMMENT	Unpublished (2004)	COMMENT	COMMENT	COMMENT	COMMENT	Unpublished (2004)	
Qy	16	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 63	ACCESSION	CN930271	EST.	ORGANISM	Malus x domestica	ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.	
Db	287	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 334	VERSION	CN930271.1	GI:48403084	REFERENCE	1 (bases 1 to 415)	REFERENCE	Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.	
RESULT 7	LOCUS	AJ876197	510 bp	mRNA	linear	EST 17-FEB-2005	DEFINITION	AJ876197 Prunus persica fruit mesocarp plus epidermis 80 days after bloom	COMMENT	Unpublished (2004)
AJ876197	DEFINITION	AJ876197 Prunus persica cDNA clone PR0213A05, mRNA sequence.	COMMENT	Unpublished (2004)	COMMENT	COMMENT	COMMENT	COMMENT	Unpublished (2004)	
Qy	16	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 63	ACCESSION	AJ876197	EST.	ORGANISM	Prunus persica (peach)	ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.	
Db	287	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 334	VERSION	AJ876197.1	GI:59932682	REFERENCE	1 (bases 1 to 510)	REFERENCE	Le Dantec,L., Cosson,P., Renaud,C., Garcia,V., Dumoulin,P., Rothan,C., Filippi,G., Laignet,F., Moing,A. and Dirlewanger,E.	
RESULT 7	LOCUS	AJ876197	510 bp	mRNA	linear	EST 17-FEB-2005	DEFINITION	AJ876197 Prunus persica fruit mesocarp plus epidermis 80 days after bloom	COMMENT	Unpublished (2004)
AJ876197	DEFINITION	AJ876197 Prunus persica cDNA clone PR0213A05, mRNA sequence.	COMMENT	Unpublished (2004)	COMMENT	COMMENT	COMMENT	COMMENT	Unpublished (2004)	
Qy	16	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 63	ACCESSION	AJ876197	EST.	ORGANISM	Prunus persica (peach)	ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.	
Db	287	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 334	VERSION	AJ876197.1	GI:59932682	REFERENCE	1 (bases 1 to 510)	REFERENCE	Le Dantec,L., Cosson,P., Renaud,C., Garcia,V., Dumoulin,P., Rothan,C., Filippi,G., Laignet,F., Moing,A. and Dirlewanger,E.	
RESULT 6	LOCUS	CN872595	498 bp	mRNA	linear	EST 04-JUN-2004	DEFINITION	0280 AAPA005328HT (AAPA) Royal Gala 24 DAFB fruit	COMMENT	Unpublished (2004)
CN872595	DEFINITION	domestica cDNA clone AAPA005328, mRNA sequence.	COMMENT	Unpublished (2004)	COMMENT	COMMENT	COMMENT	COMMENT	Unpublished (2004)	
Qy	16	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 63	ACCESSION	CN872595	EST.	ORGANISM	Malus x domestica	ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.	
Db	236	GTGGGATTGACGTAGGGCTTCCCTAGGCTATAATAGAGGGGAA 283	VERSION	CN872595.1	GI:48258753	REFERENCE	1 (bases 1 to 498)	REFERENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.	

Db	262	GGATTGACGTGAGGGTAGGGTATCTGGCTAGGCA 215		COMMENT	Contact: Gleave,A. Sequencing Facility The Horticulture and Food Research Institute of New Zealand Ltd 120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
RESULT 8				FEATURES	Tel: 00 64 09 815 4200 Fax: 00 64 09 815 4201 Email: est@hortresearch.co.nz
BH522564	BH522564	BH522564 561 bp DNA linear GSS 13-DEC-2001	source	source	
DEFINITION	DEFINITION	Brassica oleracea genomic clone BOGRW45, genomic			
VERSION	VERSION	Survey sequence.			
KEYWORDS	KEYWORDS				
ORGANISM	ORGANISM	Brassica oleracea			
REFERENCE	REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.			
AUTHORS	AUTHORS	Ayelle,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utterback,T.R., Wortsman,J.R., White,O.R., and Town,C.D.			
TITLE	TITLE	Whole genome shotgun sequencing of <i>Brassica oleracea</i> and its application to gene discovery and annotation in <i>Arabidopsis</i>			
JOURNAL	JOURNAL	Genome Res. 15 (4), 487-495 (2005)			
PUBMED	PUBMED	15805490			
COMMENT	COMMENT	Other_GSS: BOGRW45TR Contact: Chris Town			
		TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208			
		Email: cdtown@tigr.org			
		DNA is from a doubled haploid provided by Tom Osborne.			
		Seq primer: TP			
		Class: shared ends.			
FEATURES	FEATURES	Location/Qualifiers			
source	source	1..561			
		/organism="Brassica oleracea"			
		/mol type="genomic DNA"			
		/strain="RO1000DH3"			
		/db_xref="TAXON:3712"			
		/clones="BOGRW45"			
		/clone lib="BOGR"			
		/note="Vector: PHOS1; Site 1: BstXI; Site 2: 2-3 kb sheared genomic DNA inserted into _PHOS1 using BstXI linkers"			
ORIGIN	ORIGIN				
RESULT 9	RESULT 9	Query Match 50.8% Score 32; DB 9; Length 561; Best Local Similarity 79.2%; Pred. No. 1..1; Mismatches 0; Indels 0; Gaps 0;			
LOCUS	LOCUS	CN871707 598 bp mRNA linear EST 04-JUN-2004	source	source	
DEFINITION	DEFINITION	01012APAP001324HT (AAPA) Royal Gala 24 DAFB fruit <i>Malus x domestica</i> cDNA clone AAPA001324, mRNA sequence.			
ACCESSION	ACCESSION	CN871707			
VERSION	VERSION	CN871707.1 GI:48257865			
KEYWORDS	KEYWORDS	EST.			
ORGANISM	ORGANISM	Malus x domestica			
REFERENCE	REFERENCE	Malus x domestica			
AUTHORS	AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.			
TITLE	TITLE	Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., McArtney,S., Newcomb,R., Ross,G., Snowdon,K., Walton,E. and Yauk,Y.			
JOURNAL	JOURNAL	HortResearch Apple EST Project Unpublished (2004)			

Qy	16	GTGGATTGACGTGAGGGGGCTCCCTAGCTATATAGGGGAGCGAA	63		PUBMED	15805490
Db	114	GTGGATTGACGTGAGGGGGCTAGGGATGGCTATATTCTGGAGCGAA	67		COMMENT	Other_GSSs: BONLE43TR
RESULT 11						Contact: Chris Town
LOCUS	CG026604/c					TIGR
DEFINITION	PGAAE30TF	764 bp	DNA linear	GSS 19-AUG-2003		9712 Medical Center Drive, Rockville, MD 20850, USA.
SEQUENCE	CG026604					
VERSION	CG026604.1	G1:33898760				
KEYWORDS						
SOURCE	Carica papaya (papaya)					
ORGANISM	Carica papaya					
DEFINITION	Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids II; Brassicales; Caricaceae; Carica.					
REFERENCE	1 (bases 1 to 764)					
AUTHORS	Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.					
TITLE	Whole genome shotgun sequencing of Carica papaya					
JOURNAL	Unpublished (2003)					
COMMENT	Other_GSS: PGAAE30TR					
CONTACT	Chris Town					
TIGR	9712 Medical Center Drive, Rockville, MD 20850, USA.					
TEL	301-838-1523					
FAX	301-838-0208					
Email:	ctown@igr.org					
INFO	provided by Ray Ming was isolated from cultivar SunUp that was transgenic for papaya ringspot virus coat protein gene					
SEQ PRIMER	TP					
CLASS	sheared ends.					
FEATURES	source					
	1. 764					
	/organism="Carica papaya"					
	/mol type="genomic DNA"					
	/cultivar="SunUp"					
	/db_xref="PGAAE30"					
	/clone_id="PGAAE30"					
	/note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"					
ORIGIN						
DEFINITION	Query Match	50 81;	Score 32;	DB 9;	Length 825;	
SEQUENCE	Best Local Similarity	79.21;	Pred. No. 1.2;			
VERSION	Matches	38;	Conservative	0;	Indels	0;
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Arabidopsis thaliana (thale cress)					
REFERENCE	16	GTGGATTGACGTGAGGGGGCTCCCTAGGCTATAATAGGGAGCGAA	63			
AUTHORS	4	GTGGATTGACGTGAGGGGGTGTGGTAGCTATTCCTGGAGCGAA	51			
TITLE						
JOURNAL						
COMMENT						
CONTACT	Xiaoying Lin					
TIGR	The Institute for Genomic Research					
TEL	9712 Medical Center Dr., Rockville, MD 20850, USA					
EMAIL	301 838 0208					
INFO	at@igr.org					
DEFINITION	For additional information, see http://www.tigr.org/cdb/at/at.html					
SEQUENCE						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids II; Brassicales; Brassicaceae; Brassica.					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	BONLE43TR BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
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SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
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SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
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SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					
VERSION	1 (bases 1 to 825)					
KEYWORDS						
SOURCE						
ORGANISM						
DEFINITION	Brassica oleracea					
SEQUENCE	AY814375 BO 1-6 2 KB tot Brassica oleracea genomic clone BONLE43,					

Query Match	48.3%	Score 30.4; DB 9; Length 169;	REFERENCE	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
Best Local Similarity	77.1%	Pred. No. 3.8;	AUTHORS	1 (bases 1 to 194) Bueli, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T., and Fraser, C.M.
Matches	37;	Conservative 0; Mismatches 11; Indels 0; Gaps 0;	TITLE	Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms
Qy	16	GTGGATTGACGTGAGGGGCCCTAGCTATATTAGGGAGCGAA 63	JOURNAL	Unpublished (2000)
Db	118	GTGGATTGACGTGAGGGCTAGCTATATTAGGGAGCGAA 71	COMMENT	Contact: Xiaoying Lin The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Email: at@tigr.org
RESULT 14				For additional information, see http://www.tigr.org/tdb/at/at.html
B2483881	B2483881	183 bp DNA linear GSS 13-DEC-2002	FEATURES	
LOCUS	BOA129TR BO 1	6.2 KB rot Brassica oleracea genomic clone BOA129,	source	1. organism="Arabidopsis thaliana"
DEFINITION		Genomic survey sequence.		/mol type="genomic DNA"
ACCESSION	B2483881	GI:26786279		/ecotype="Landsberg erecta"
VERSION				/db xref="Taxon:3702"
KEYWORDS				/clone="LBRG145"
SOURCE	Brassica oleracea			/clone lib="LBRG"
ORGANISM	Brassica oleracea			/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4-0.7 kbp before ligation."
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.		ORIGIN	Query Match 48.3%; Score 30.4; DB 9; Length 194;
REFERENCE				Best Local Similarity 77.1%; Pred. No. 3.9;
AUTHORS	Ayelle, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Worsham, J.R., White, O.R., and Town, C.D.		Matches 37; Conservative 0; Mismatches 11; Indels 0; Gaps 0;	
TITLE	Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis			Qy 16 GTGGATTGACGTGAGGGCTCCCTAGGCTATATTAGGGAGCGAA 63
JOURNAL	Genome Res. 15 (4), 487-495 (2005)			Db 137 GTGGATTGACGTGAGGGTAGGTAGGGTAGCTATTCTGGGAGCGAA 90
PUBLISHED	15805490			Search completed: February 21, 2006, 07:16:42
COMMENT	Other GSSs: BOA129TR			Job time : 3776 secs
	Contact: Chris Town			
	TIGR			
	9712 Medical Center Drive, Rockville, MD 20850, USA.			
	Tel: 301-838-3523			
	Fax: 301-838-0208			
	Email: ctown@tigr.org			
	DNA is from a doubled haploid provided by Tom Osborn.			
	Seq primer: "TR			
	Class: sheared ends.			
FEATURES	source	Location/Qualifiers		
	1..183			
	/organism="Brassica oleracea"			
	/mol type="genomic DNA"			
	/strain="TOL0000DH3"			
	/db xref="Taxon:3712"			
	/clone=BOA129"			
	/clone lib="BO 1..6.2 KB tot"			
	/note="Vector: pHO51; Site:1; BstXI: 1..6..2 kb sheared total DNA inserted into pho51 using BstXI linkers"			
ORIGIN				
Query Match	48.3%	Score 30.4; DB 9; Length 183;		
Best Local Similarity	77.1%	Pred. No. 3.9;		
Matches	37;	Conservative 0; Mismatches 11; Indels 0; Gaps 0;		
Qy	16	GTGGATTGACGTGAGGGCTCCCTAGGCTATATTAGGGAGCGAA 63		
Db	62	GTGGATTGACGTGAGGGTAGGTAGCTATTCTGGGAGCGAA 109		
RESULT 15				
LOCUS	AQ962945	194 bp DNA linear GSS 28-JAN-2000		
DEFINITION	LERG145TR LBRG Arabidopsis thaliana genomic clone LBRG145, genomic survey sequence.			
ACCESSION	AQ962945			
VERSION	AQ962945..1	GI:6790646		
KEYWORDS	GSS			
ORGANISM	Arabidopsis thaliana (thale cress)			
	Arabidopsis thaliana			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;			

Database : N_Geneseq_21:*

ALIGNMENTS

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2:  geneseqn1990s: *
3:  geneseqn2000s: *
4:  geneseqn2001as: *
5:  geneseqn2001bs: *
6:  geneseqn2002as: *
7:  geneseqn2002bs: *
8:  geneseqn2003as: *
9:  geneseqn2003bs: *
10: geneseqn1003cs: *
11: geneseqn2003ds: *
12: geneseqn2004as: *
13: geneseqn1004bs: *
14: geneseqn2005s: *

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IMMAPTEC

Result No.	Score	Query	Match	Length	DB	ID	Description	
							Pr	Adt
1	63	100.0	63	13	ADT78252		78352	Mutant
2	38.4	61.0	112	13	ADT78220		78220	DNA sequ
3	38.4	61.0	112	13	ADT78224		78224	DNA sequ
4	38.4	61.0	112	13	ADT78219		78219	DNA sequ
5	36.6	58.1	112	13	ADT78211		78211	DNA sequ
6	34.8	55.2	112	13	ADT78210		78210	DNA sequ
7	33.6	53.3	91	9	ACCB85363		85363	N tabacum
8	33.6	53.3	91	10	ADB34206		34206	Tobacco P
9	33.6	53.3	112	13	ADT78229		78229	DNA sequ
10	33.6	53.3	112	13	ADT78231		78231	DNA sequ
11	33.6	53.3	112	13	ADT78228		78228	DNA sequ
12	33.6	53.3	112	13	ADT78230		78230	DNA sequ
13	33.6	53.3	112	13	ADT78207		78207	DNA sequ
14	33.6	53.3	112	13	ADT78204		78204	DNA sequ
15	33.6	53.3	112	13	ADT78208		78208	DNA sequ
16	33.6	53.3	112	13	ADT78206		78206	DNA sequ
17	33.6	53.3	112	13	ADT78205		78205	DNA sequ
18	33.6	53.3	112	13	ADT78209		78209	DNA sequ
19	33.6	53.3	113	14	ADP36357		36357	Oligonucleic

RESULT 1
 ADT78852
 ID ADT78252 standard; DNA: 63 BP.
 XX
 AC ADT78252;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE Mutant Prrn promoter (Prn1) useful for transgene expression in plants.
 XX
 KW Heterologous molecule expression; plastid rRNA operon; Prrn promoter;
 KW transgenic plant; transgene expression; chimera promoter; mutant;
 KW promoter; transgene; mutant; chimera promoter; mutant;
 KW promoter; transgene; mutant; chimera promoter; mutant;

XX	04 -NOV-2004 .
PD	
XX	15 -DEC-2003 ; 2003US-00737251 .
PF	
XX	13 -DEC-2002; 2002US-0433302P .
PR	
XX	(MALI/) MALIGA P .
PA	(SUZU/) SUZUKI J Y .
PA	
XX	Maliga P , Suzuki JY ;
PI	
XX	WPI : 2004 -774976/76 .
DR	
XX	New isolated nucleic acid seq
PT	heterologous molecules in the
PT	constructing chimeric promote
PT	
XX	Claim 7 ; SEQ ID NO 51 ; 34pp ;
PS	
XX	The invention relates to nucleic
CC	acid sequences of heterologous molecules in
CC	the invention relates to nucleic
CC	acid sequences are selected for

given as SEQ ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (given as SEQ ID No: 51). Also disclosed are: (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising this vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transcription modulating element (PTME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased relative to that observed using wild-type Prrn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins in plastids. The present sequence represents a mutant Prrn promoter that can be used to express heterologous molecules in the plastids of higher plants.

XX Sequence 63 BP; 13 A; 12 C; 24 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 63; DB 13; Length 63;
Best Local Similarity 100.0%; Pred. No. 8.1e-14;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAGCTCTTCAGGGCTGGATGACGTTGAGGGCTCCCTAGGCTATTAGGGAGC 60
Db 1 GAGCTCTTCAGGGCTGGATGACGTTGAGGGCTCCCTAGGCTATTAGGGAGC 60

Qy 61 GAA 63

Db 61 GAA 63

RESULT 2
ADT78220
ID ADT78220 standard; DNA; 112 BP.
XX AC
XX DT 27-JAN-2005 (first entry)
XX DE DNA sequence of Prrn promoter derivative pJYS172.

XX Heterologous molecule expression; Plastid rRNA operon; Prrn promoter;
XX transgenic plant; transgene expression; PTME; chimeric promoter; ds.
XX Unidentified.
XX OS US2004221338-A1.
XX PR 13-DEC-2002; 2002US-0433302P.
XX PD 04-NOV-2004.
XX PF 15-DEC-2003; 2003US-00737251.
XX PR 13-DEC-2002; 2002US-0433302P.

XX PA (MALI/) MALIGA P.
XX PA (SUZU/) SUZUKI J Y.
XX PI Maliga P, Suzuki JY;
XX DR 2004-774976/76.
XX PS New isolated nucleic acid sequence, useful for promoting expression of
PT heterologous molecules in the plastids of higher plants and for
PT constructing chimeric promoters for transgene expression.
XX PS Claim 1; SEQ ID NO 19; 34pp; English.

XX The invention relates to nucleic acid sequences for promoting expression
CC of heterologous molecules in the plastids of higher plants. The nucleic
CC acid sequences are selected from plastid rRNA operon (Prrn) sequences
CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
CC mutations which minimise homologous recombination at the Prrn operon
CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
CC nucleic acid sequence above, (b) a transgenic plant comprising this
CC vector, (c) a chimeric promoter for expression of transgenes in plastids
CC of higher plants, comprising at least one Prrn transcription modulating
CC element (PTME) operably linked to a promoter element, the chimeric
CC promoter being further operably linked to a sequence encoding a
CC heterologous molecule of interest, and (d) a vector comprising the
CC chimeric promoter. The nucleic acid sequence is operably linked to a
CC sequence encoding a heterologous molecule of interest or its precursor.
CC Expression of the heterologous molecule is decreased or increased
CC relative to that observed using wild-type Prrn sequence. The nucleic acid
CC sequence is useful for constructing chimeric promoters for transgene
CC expression and for driving high level expression of heterologous proteins
CC in plastids. The present sequence represents a Prrn promoter derivative.
XX SQ Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;

Query Match 61.0%; Score 38.4; DB 13; Length 112;
Best Local Similarity 87.5%; Pred. No. 0.0016;
Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 16 GTGGGATTGACCTGAGGGGGTCTCCCTAGGCTATATAGGGAGCGAA 63
Db 28 GTGGGATTGACCTGAGGGGGTCTCCCTAGGCTATATAGGGAGCGAA 75
RESULT 3
ADT78224
ID ADT78224 standard; DNA; 112 BP.
XX AC
XX DT 27-JAN-2005 (first entry)
XX DE DNA sequence of Prrn promoter derivative pJYS176.
XX KW Heterologous molecule expression; Plastid rRNA operon; Prrn promoter;
KW transgenic plant; transgene expression; PTME; chimeric promoter; ds.
XX KW Prrn transcription modulating element; PTME; chimeric promoter; ds.
XX OS Unidentified.
XX PN US2004221338-A1.
XX PR 13-DEC-2002; 2002US-0433302P.
XX DR 2004-774976/76.
XX PA (MALI/) MALIGA P.
XX PA (SUZU/) SUZUKI J Y.
XX PI Maliga P, Suzuki JY;
XX DR 2004-774976/76.
XX PS New isolated nucleic acid sequence, useful for promoting expression of
PT heterologous molecules in the plastids of higher plants and for
PT constructing chimeric promoters for transgene expression.
XX PS Claim 1; SEQ ID NO 19; 34pp; English.
XX The invention relates to nucleic acid sequences for promoting expression
CC of heterologous molecules in the plastids of higher plants. The nucleic
CC acid sequences are selected from plastid rRNA operon (Prrn) sequences
CC given as SEQ ID Nos: 4-30 in the specification, or which may comprise
CC mutations which minimise homologous recombination at the Prrn operon
CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
CC nucleic acid sequence above, (b) a transgenic plant comprising this

vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transcription modulating element (PTrME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased relative to that observed using wild-type Prrn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins in plastids. The present sequence represents a Prrn promoter derivative.

Sequence 112 BP; 33 A; 16 C; 42 G; 21 T; 0 U; 0 Other;
 Query Match 61.0%; Score 38.4%; DB 13; Length 112;
 Best Local Similarity 87.5%; Pred. No. 0.00016;
 Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 16 GTGGGATTGAGCTGAGGGGGTCCCTAGGCTATAATTAGGGAGGCGAA 63
 Db 28 GTGGGATTGAGCTGAGGGGGTCCCTAGGCTATAATTAGGGAGGCGAA 75

RESULT 4
 ID ADT8219 standard; DNA; 112 BP.
 XX
 AC ADT8219;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE DNA sequence of Prrn promoter derivative PTrS171.
 XX
 KW Heterologous molecule expression; Plastid rRNA operon; Prrn promoter;
 KW Transgenic Plant; transgene expression; PTME; chimeric promoter; ds.
 XX
 OS Unidentified.
 XX
 PN US2004221338-A1.
 XX
 PD 04-NOV-2004.
 XX
 PF 15-DEC-2003; 2003US-00737251.
 XX
 PR 13-DEC-2002; 2002US-0433302P.
 XX
 PA (MALI/) MALIGA P.
 PA (SUZU/) SUZUKI J Y.
 PI Maliga P, Suzuki JY;
 XX
 DR WPI; 2004-774976/76.
 XX
 PS SEQ ID NO 10; 34pp; English.

PT New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.
 XX
 PT Claim 1; SEQ ID NO 18; 34pp; English.
 XX
 The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences given as SEQ ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising this vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transcription modulating element (PTME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the

chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased relative to that observed using wild-type Prrn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins in plastids. The present sequence represents a Prrn promoter derivative.

Sequence 112 BP; 30 A; 19 C; 39 G; 24 T; 0 U; 0 Other;
 Query Match 61.0%; Score 38.4%; DB 13; Length 112;
 Best Local Similarity 87.5%; Pred. No. 0.00016;
 Matches 42; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 16 GTGGGATTGAGCTGAGGGGGTCCCTAGGCTATAATTAGGGAGGCGAA 63
 Db 28 GTGGGATTGAGCTGAGGGGGTCCCTAGGCTATAATTAGGGAGGCGAA 75

RESULT 5
 ID ADT8211
 XX
 AC ADT8211;
 XX
 DT 27-JAN-2005 (first entry)
 XX
 DE DNA sequence of Prrn promoter derivative PTrS119.
 XX
 KW Heterologous molecule expression; plastid rRNA operon; Prrn promoter;
 KW Transgenic plant; transgene expression; PTME; chimeric promoter; ds.
 XX
 OS Unidentified.
 XX
 PN US2004221338-A1.
 XX
 PD 04-NOV-2004.
 XX
 PF 15-DEC-2003; 2003US-00737251.
 XX
 PR 13-DEC-2002; 2002US-0433302P.
 XX
 PA (MALI/) MALIGA P.
 PA (SUZU/) SUZUKI J Y.
 PI Maliga P, Suzuki JY;
 XX
 DR WPI; 2004-774976/76.
 XX
 PS SEQ ID NO 10; 34pp; English.

PT New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.
 XX
 PT The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences given as SEQ ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising this vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transcription modulating element (PTME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased relative to that observed using wild-type Prrn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene

CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a *Prnr* promoter derivative.
 XX

SQ Sequence 112 BP; 32 A; 15 C; 43 G; 22 T; 0 U; 0 Other;
 XX

Query Match 58.1%; Score 16.6; DB 13; Length 112;
 Best Local Similarity 82.4%; Pred. No. 0.00074;
 Matches 42; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 DB 25 GAGGTGGATTGACGTGAGGGGGCTCCCTAGGCTATTTAGGGACGCCA 63
 25 GAGGTGGATTGACGTGAGGGGGCAAGGGATGGCTATTTCTGGAGCGAA 75

RESULT 6
 ADT78210
 ID ADT78210 standard; DNA; 112 BP.
 XX

AC ADT78210;
 XX

DT 27-JAN-2005 (first entry)
 XX

DE DNA sequence of *Prnr* promoter derivative pJY118.
 XX

XX Heterologous molecule expression; plastid rRNA operon; *Prnr* promoter;
 KW transgenic plant; transgene expression;
 KW *Prnr* transcription modulating element; PTME; chimeric promoter; ds.
 XX Unidentified.
 OS US2001221338-A1.
 XX

PN 04-NOV-2004.
 XX

PD 15-DEC-2003; 2003US-00737351.
 XX

PR 13-DEC-2002; 2002US-04333302P.
 XX

XX (MALI) MALIGA P.
 PA (SUZU) SUZUKI J Y.
 XX

PI Maliga P, Suzuki JY;
 XX

PR 2004-774976/76.
 XX

XX New isolated nucleic acid sequence, useful for promoting expression of
 PT heterologous molecules in the plastids of higher plants and for
 PR constructing chimeric promoters for transgene expression.
 XX

PS Claim 1; SEQ ID NO 9; 34pp; English.
 XX

XX The invention relates to nucleic acid sequences for promoting expression
 CC of heterologous molecules in the plastids of higher plants. The nucleic
 CC acid sequences are selected from plastid rRNA operon (Prnr) sequences
 CC given as SEQ ID Nos: 4-30 in the specification or which may comprise
 CC mutations which minimise homologous recombination at the *Prnr* operon
 CC (given as SEQ ID No: 51). Also disclosed are (a) a vector comprising the
 CC nucleic acid sequence above, (b) a transgenic plant comprising this
 CC vector, (c) a chimeric promoter for expression of transgenes in plastids
 CC of higher plants, comprising at least one *Prnr* transcription modulating
 CC element (PTME) operably linked to a promoter element, the chimeric
 CC promoter being further operably linked to a sequence encoding a
 CC chimeric promoter. The nucleic acid sequence is operably linked to a
 CC sequence encoding a heterologous molecule of interest or its precursor.
 CC Expression of the heterologous molecule is decreased or increased
 CC relative to that observed using wild-type *Prnr* sequence. The nucleic acid
 CC sequence is useful for constructing chimeric promoters for transgene
 CC expression and for driving high level expression of heterologous proteins
 CC in plastids. The present sequence represents a *Prnr* promoter derivative.
 XX

SQ Sequence 112 BP; 30 A; 19 C; 39 G; 24 T; 0 U; 0 Other;

Query Match 55.2%; Score 34.8; DB 13; Length 112;
 Best Local Similarity 77.8%; Pred. No. 0.035; Mismatches 12; Indels 0; Gaps 0;
 Matches 42; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 10 TCCGAGGTGGATTGACGTGAGGGGGCTCCCTAGGCTATTTAGGGAGCGAA 63
 DB 22 TCCCTGGATTGACGTGAGGGATGGCTATTTCTGGAGCGAA 75

RESULT 7
 ACC85363
 ID ACC85363 standard; DNA; 91 BP.
 XX

AC ACC85363;
 XX

DT 18-SEP-2003 (first entry)
 XX

DE N tabacum *Prnr16* promoter.
 XX

KW Vegetable plastid transformation; transgenic; recognition sequence;
 KW plant; site-specific integration; nutrition; seed production; gene;
 KW chemical production; promoter; ds.
 XX

OS Nicotiana tabacum.
 PN WO2003054201-A1.
 XX

PD 03-JUL-2003.
 XX

PP 16-DEC-2002; 2002WO-EP014303.
 XX

PR 20-DEC-2001; 2001DE-01063159.
 XX

PA (SUNG-) SUNGENE GMBH & CO KGAA.
 XX

PI Biesgen C;
 XX

DR WPI; 2003-541820/51.
 XX

PT Site-specific integration of DNA into plastid DNA, useful for making
 PT transgenic plants used e.g. as food, by recombinase-mediated insertion.
 XX

PS Disclosure; Page 132; 164pp; German.
 XX

CC The present invention relates to a method for the site-specific
 CC integration of a DNA sequence into the plastid DNA of a plant or its
 CC derived cells. Transgenic plant in which a DNA sequence has been
 CC integrated, also their cell cultures, tissues etc. are useful in
 CC human or animal nutrition, to produce seeds, and to produce
 CC pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids,
 CC flavourings and aromatizing agents, dyes, antibodies and vaccines. The
 CC present sequence is a gene fragment shown in the exemplification of the
 CC invention

SQ Sequence 91 BP; 20 A; 16 C; 36 G; 19 T; 0 U; 0 Other;
 XX

Query Match 53.3%; Score 33.6; DB 9; Length 91;
 Best Local Similarity 81.2%; Pred. No. 0.0096; Mismatches 9; Indels 0; Gaps 0;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 16 GTCGGATTGACGTGAGGGGGCTCCTAGGCTATTTAGGGAGCGAA 63
 DB 34 GTCGGATTGACGTGAGGGGGCTCCTAGGCTATTTAGGGAGCGAA 81

RESULT 8
 ADB34206
 ID ADB34206 standard; DNA; 91 BP.
 XX

AC ADB34206;
 XX

DT 29-JAN-2004 (first entry)
 XX

DE	Tobacco Prnr6 promoter DNA.	XX	XX	XX	DT	27-JAN-2005	(first entry)
KW	plastid; plant; homotransplastomic cell; insertion sequence; nutrition;	XX	XX	XX	DE	DNA sequence of Prnr promoter derivative pJYS181.	
KW	seed production; enzyme; vitamin; amino acid; flavouring;	XX	XX	XX			
KW	aromatising agent; dye; antibody; vaccine; ds.	XX	XX	XX			
XX	Nicotiana tabacum.	OS	OS	OS			
XX	WO2003054189-A2.	PN	PN	PN			
XX	03-JUL-2003.	PD	PD	PD			
XX	PR 16-DEC-2002; 2002WO-EP014302.	XX	XX	XX			
PR	20-DBC-2001; 2001DE-01063161.	XX	XX	XX			
PA	(SUNGNE-) SUNGENE GMBH & CO KGAA.	XX	XX	XX			
PI	Biesgen C;	XX	XX	XX			
DR	WPI; 2003-541816/51.	XX	XX	XX			
PT	Method for integrating DNA into plant plastids, useful for making	XX	XX	XX			
PT	transgenic plants for e.g. food or animal feed, by inducing targeted	XX	XX	XX			
PT	double-strand DNA breaks.	XX	XX	XX			
PS	Disclosure; SEQ ID NO 46; 182pp; German.	XX	XX	XX			
CC	This invention describes a novel method for integrating a DNA sequence	CC	CC	CC			
CC	into the plastid DNA of a multicellular plant or its derived cells and	CC	CC	CC			
CC	for selecting homotransplastomic cells or plants. The method comprises	CC	CC	CC			
CC	inducing DNA double-strand breaks in plant plastid DNA, which contains at	CC	CC	CC			
CC	least one recognition site for targeted induction of such breaks, by	CC	CC	CC			
CC	treating the plastid DNA with an enzyme able to create these	CC	CC	CC			
CC	breaks and a transformation construct that contains an insertion sequence	CC	CC	CC			
CC	which is inserted into the plastid DNA so that the function of the	CC	CC	CC			
CC	recognition site for targeted induction of breaks is inactivated, i.e. it	CC	CC	CC			
CC	is no longer cleaved by the enzyme. Plants or cells in which the	CC	CC	CC			
CC	insertion sequence has been inserted are then selected. Transgenic plants	CC	CC	CC			
CC	in which the DNA sequence has been integrated, and also their cell	CC	CC	CC			
CC	cultures, organs, tissues, are useful in human or animal nutrition, for	CC	CC	CC			
CC	producing seeds, and pharmaceuticals or fine chemicals, e.g. enzymes,	CC	CC	CC			
CC	vitamins, amino acids, flavourings and aromatising agents, dyes,	CC	CC	CC			
CC	antibodies and vaccines. The method eliminates the need for	CC	CC	CC			
CC	antibiotic/hercicide selection markers and ensures efficient integration	CC	CC	CC			
CC	of foreign DNA into all copies of plastid DNA, also effective selection,	CC	CC	CC			
CC	so provides a quicker, more efficient and less expensive method of	CC	CC	CC			
CC	producing homotransplastomic plants. The genetic constructs used are	CC	CC	CC			
CC	small, since only short homology regions are required. Double-crossover	CC	CC	CC			
CC	events occur easily in plastid DNA, at specific locations, avoiding the	CC	CC	CC			
CC	problems of gene silencing associated with recombination in the nucleus	CC	CC	CC			
CC	and high level expression can be achieved, because of the high copy	CC	CC	CC			
CC	number of plastid DNA. Foreign DNA will not be transferred in pollen	CC	CC	CC			
CC	(inheritance of plastid DNA is maternal) and since plastids resemble	CC	CC	CC			
CC	prokaryotes, they can express several genes from polycistronic operons,	CC	CC	CC			
CC	under control of a single promoter.	XX	XX	XX			
SO	Sequence 91 BP; 20 A; 16 C; 36 G; 19 T; 0 U; 0 Other;	XX	XX	XX			
Qy	Query Match 53.1%; Score 33.6%; DB 10; Length 91;	Best Local Similarity 81.2%; Pred. No. 0.0056; Mismatches 0; Gaps 0;	Qy	16 GTGGGATTGAGCTGAGGGGGCTCCCTAGGCTATAATTAGGGAGCGAA 63	RESULT 10		
Db	Matches 39; Conservative 0; Mismatches 9; Gaps 0;	DB	DB	17 ADT78231 standard; DNA; 112 BP.	ADT78231	DT	27-JAN-2005 (first entry)
XX	34 GTGGGATTGAGCTGAGGGGGAGGATGGCTATAATTCTGGAGCGAA 81	XX	XX	28 ADT78231 standard; DNA; 112 BP.	ADT78231	DE	DNA sequence of Prnr promoter derivative pJYS183.
XX	RESULT 9	AC	AC	ADT78229	ADT78229		
XX	ID ADT78229 standard; DNA; 112 BP.	XX	XX				

PF	15-DEC-2003 ; 2003US-00737251.	PA (SUZU/) SUZUKI J Y.
XX	PR 13-DEC-2002 ; 2002US-0433302P.	XX PI Maliga P, Suzuki JY;
XX	PA (MALI/) MALIGA P.	XX DR WPI; 2004-774976/76.
PA (SUZU/) SUZUKI J Y.	XX PT New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.	XX PT PT PT
XX	PI Maliga P, Suzuki JY;	XX PT constructing chimeric promoters for transgene expression.
XX	DR 2004-774976/76.	XX PS Claim 1: SEQ ID NO 6; 34pp; English.
XX	XX	XX The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences given as SEQ ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (given as SEQ ID NO: 51). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising this vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transcription modulating element (PTME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased relative to that observed using wild-type Prrn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins in plastids. The present sequence represents a Prrn promoter derivative.
PS	SEQ ID NO 29; 34pp; English.	XX SQ Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;
XX	XX	XX Query Match 53.3%; Score 33.6; DB 13; Length 112; Best Local Similarity 81.2%; Pred. No. 0.01; Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
XX	XX	XX Qy 16 GTGGGATTGAGCTAGGGGCTCCCTAGGCTATAATTAGGGAGGAA 63 Db 28 GTGGGATTGAGCTAGGGGCTCCCTAGGCTATAATTAGGGAGGAA 75
XX	XX	XX RESULT 14 ADT78204 standard; DNA; 112 BP.
SQ	Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;	XX DT 27-JAN-2005 (first entry) ADT78204
XX	XX	XX DE DNA sequence of Prrn promoter derivative pJYS112.
XX	XX	XX AC ADT78207; DE
XX	XX	XX KW Heterologous molecule expression; plastid rRNA operon; Prrn promoter; KW transgenic plant; transgene expression; PTME; chimeric promoter; ds. KW Prrn transcription modulating element; PTME; chimeric promoter; ds. KW Unidentified. KW OS Unidentified.
XX	XX	XX PR 13-DEC-2002; 2002US-0433302P.
XX	XX	XX XX US2004221338-A1. XX PD 04-NOV-2004.
XX	XX	XX PA (MALI/) MALIGA P. PA (SUZU/) SUZUKI J Y.
XX	XX	XX PR 15-DEC-2003; 2003US-00737251. PA (SUZU/) SUZUKI J Y.
XX	XX	XX PR 13-DEC-2002; 2002US-0433302P.
PA	PA (MALI/) MALIGA P.	XX DR 2004-774976/76.

New isolated nucleic acid sequence, useful for promoting expression of heterologous molecules in the plastids of higher plants and for constructing chimeric promoters for transgene expression.

Disclosure: SEQ ID NO 3; 34pp; English.

The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from Plastid rRNA Operon (Prnr) sequences given as SEQ ID Nos: 4-10 in the specification, or which may comprise mutations which minimize homologous recombination at the Prnr operon (given as SEQ ID No: 5). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising this vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prnr transcription modulating element (PME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased relative to that observed using wild-type Prnr sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins in plastids of higher plants.

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K Sequence 112 BP; 31 A; 17 C; 41 G; 23 T; 0 U; 0 Other;
Q Query Match 53.3%; Score 33.6; DB 13; Length 112;
B Best Local Similarity 81.2%; Pred. No. 0.01;
M Matches 39; Conservative 0; Mismatches 9; Indels 0; gaps 0;
Y 16 GTGGGATTACGTTAGGGCTTCCCTAGGCTATATAGGGAGCGA 63
Y 28 GTGGGATTACGTTAGGGCTTCCCTAGGCTATATAGGGAGCGA 75

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PS Claim 1; SEQ ID NO 7; 340pp; English.

XX The invention relates to nucleic acid sequences for promoting expression of heterologous molecules in the plastids of higher plants. The nucleic acid sequences are selected from plastid rRNA operon (Prrn) sequences given as SEQ ID Nos: 4-30 in the specification, or which may comprise mutations which minimise homologous recombination at the Prrn operon (Given as SEQ ID NO: 51). Also disclosed are (a) a vector comprising the nucleic acid sequence above, (b) a transgenic plant comprising this vector, (c) a chimeric promoter for expression of transgenes in plastids of higher plants, comprising at least one Prrn transcription modulating element (PrTME) operably linked to a promoter element, the chimeric promoter being further operably linked to a sequence encoding a heterologous molecule of interest, and (d) a vector comprising the chimeric promoter. The nucleic acid sequence is operably linked to a sequence encoding a heterologous molecule of interest or its precursor. Expression of the heterologous molecule is decreased or increased relative to that observed using wild-type Prrn sequence. The nucleic acid sequence is useful for constructing chimeric promoters for transgene expression and for driving high level expression of heterologous proteins in plastids. The present sequence represents a Prrn promoter derivative.

XX Sequence 112 BP; 31 A; 18 C; 40 G; 23 T; 0 U; 0 Other;

SQ Query Match 53-34; Score 33.6; DB 13; Length 112;
Best Local Similarity 81.2%; Pred. No. 0-01; Mismatches 0; Indels 0; Gaps 0;

Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 16 GGGGATTTGACCTGAGGGGGCCCTAGCTATATAGGGGAGGCGAA 63
DB 28 GTGGGATTTGACCTGAGGGGGCCCTAGCTATATAGGGGAGGCGAA 75

RESULT 15
 DDT78208 standard; DNA: 112 BP.
 X ADT78208;
 X X
 X 27-JAN-2005 (first entry)
 X X DNA sequence of *Prnr* promoter derivative pJYS116.
 X X Heterologous molecule expression; plastid rRNA operon
 X X transgenic plant; transgene expression; PTME; chimeric
 X X *Prnr* transcription modulating element;
 X X Unidentified.
 X X US2004221338-A1.
 X X 04-NOV-2004.
 D D 15-DEC-2003; 2003US-00737251.
 F F 13-DEC-2002; 2002US-0433302P.
 X X (MALI/) MALIGA P.
 X A (SUZU/) SUZUKI J Y.
 X X Maligna P, Suzuki JY;
 R R WPI; 2004-774976/76.
 X X New isolated nucleic acid sequence, useful for promoting
 X T heterologous molecules in the plastids of higher plants;
 X T constructing chimeric promoters for transgene expression.

ALIGNMENTS

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OPICIN promoter 1. 91 /note="plastidic promoter Prrn16"

RESULT 2	AX79854	AX798954	Sequence 46 from Patent WO03054189.	91 bp	DNA	PAT 08-OCT-2003
LOCUS	DEFINITION	Sequence 46 from Patent WO03054189.				
ACCESSION	VERSION	AX798954	AX798954	1	GT-7750500000	

KEYWORDS	Nicotiana tabacum (common tobacco)
SOURCE	Nicotiana tabacum
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE	¹ Biesgen, C. Methods for the transformation of vegetal plastids Patent: WO 03054189-A 46 03-JUL-2003; Sungene GmbH & Co. KGaA (DE)
FEATURES	source
AUTHORS	1. .91
TITLE	/organism="Nicotiana tabacum"
JOURNAL	/mol type="unassigned DNA"
Db	/db_xref="taxon:4097"
promoter	1. .91
	/note="plastidic promoter Prn16"
ORIGIN	
Query Match	53.3%; Score 33.6; DB 6; Length 91;
Best Local Similarity	81.2%; Pred. No. 0.097;
Matches	39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy	16 GTGGATTGACTGAGGGCTCCTAGGCTATATTAGGGAGCGAA 63
Db	34 GTGGATTGACTGAGGGAGGGATGGCTATTTCTGGAGCGAA 81
RESULT 3	
CS114516	CS114516 CS114516 CS114516
LOCUS	113 bp DNA
DEFINITION	Sequence 13 from Patent WO2005054481.
ACCESSION	CS114516
VERSION	GI:68226041
KEYWORDS	synthetic construct
SOURCE	synthetic construct
ORGANISM	other sequences; artificial sequences.
REFERENCE	
AUTHORS	1. MUEHLBAUER, S.
TITLE	Controlling gene expression in plastids Patent: WO 2005054481-A 13 16-JUN-2005;
JOURNAL	Icon Genetics AG (DE)
Db	/note="cloning oligo"
FEATURES	source
AUTHORS	1. .113
TITLE	/organism="synthetic construct"
JOURNAL	/mol type="unassigned DNA"
Db	/db_xref="taxon:32830"
ORIGIN	
Query Match	53.3%; Score 33.6; DB 6; Length 113;
Best Local Similarity	81.2%; Pred. No. 0.097;
Matches	39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy	16 GTGGATTGACTGAGGGCTCCTAGGCTATATTAGGGAGCGAA 63
Db	38 GTGGATTGACTGAGGGAGGGATGGCTATTTCTGGAGCGAA 85
RESULT 4	
CS001461	CS001461 CS001461
LOCUS	119 bp DNA
DEFINITION	Sequence 6 from Patent WO200505643.
VERSION	CS001461
KEYWORDS	Nicotiana tabacum (common tobacco)
SOURCE	Nicotiana tabacum
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.
RESULT 4	
CS001461	CS001461 CS001461
LOCUS	119 bp DNA
DEFINITION	Sequence 6 from Patent WO200505643.
VERSION	CS001461
KEYWORDS	Nicotiana tabacum (common tobacco)
SOURCE	Nicotiana tabacum
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.
RESULT 5	
CS11179	CS11179 CS11179
LOCUS	127 bp DNA
DEFINITION	Method for transforming plant and transformed plant.
VERSION	JP 2001046073-A/16.
KEYWORDS	Nicotiana tabacum (common tobacco)
ORGANISM	Nicotiana tabacum
REFERENCE	
AUTHORS	1. Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.
TITLE	Method for transforming plant and transformed plant
JOURNAL	RIKAGAKU KENKYUSHO, HIDEO NAKASHITA
COMMENT	OS Nicotiana tabacum (tobacco)
PD	20-FEB-2001
PR	09-AUG-1999 JP 1999225832
PC	PI HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIHARU DOI C12N15/09, A01H5/00, C12N9/10, C12N9/02, C12N9/10, C12P7/62, PC
CC	C12N15/00, C12N5/00
CC	CC Key
PH	Location/Qualifiers
FT	1. .127
FT	/organism='Nicotiana tabacum (tobacco)'.
FEATURES	source
ORIGIN	
Query Match	53.3%; Score 33.6; DB 6; Length 127;
Best Local Similarity	81.2%; Pred. No. 0.097;
Matches	39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
Qy	16 GTGGATTGACTGAGGGCTCCTAGGCTATATTAGGGAGCGAA 63
Db	53 GTGGATTGACTGAGGGAGGGATGGCTATTTCTGGAGCGAA 100
RESULT 6	
CS11197	CS11197 CS11197
LOCUS	127 bp DNA
DEFINITION	Process for producing polyester.
ACCESSION	ES11197
KEYWORDS	JP 2001046074-A/16.

SOURCE	Nicotiana tabacum (common tobacco)	DEFINITION	Sequence 16 from Patent EP1076095.
ORGANISM	Nicotiana tabacum	ACCESSION	AX137514
	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eu dicotyledons; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Nicotiana.	VERSION	AX137514.1
REFERENCE	1 (bases 1 to 127)	KEYWORDS	Nicotiana tabacum (common tobacco)
AUTHORS	Nakashita, H., Yamaguchi, I., Yoshioka, K. and Doi, Y.	ORGANISM	Nicotiana tabacum
TITLE	Process for Producing Polyester	FEATURES	Streptophyta; Embryophyta; Tracheophyta; core eudicotyledons; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
JOURNAL	Patent: JP 2001046074 A 16 20-FEB-2001; RI KAGAKU KENKYUSHO	REFERENCE	
COMMENT	OS Nicotiana tabacum (tobacco)	AUTHORS	Yamaguchi, I., Nakashita, H., Yoshioka, K. and Doi, Y.
PN	JP 2001046074-A/16	TITLE	Methods for transformation of plants, transformed plants and processes for preparation of polyesters
PD	20-FEB-2001	JOURNAL	Patent: EP 1076095-A 16 14-FEB-2001; Riken (JP)
PF	09-AUG-1999	FEATURES	Location/Qualifiers
PR	JP 1999225839	source	1. .127 /organism="Nicotiana tabacum" /mol_type="unassigned DNA" /db_xref="#taxon:4097"
PI	HIDEO NAKASHITA, ISAMU YAMAGUCHI, KEIKO YOSHIOKA, YOSHIHARU DOI	ORIGIN	
PC	PC C12N15/09 A01H5/00, C12N5/10, C12N9/02, C12N9/10, C12P7/62, PC C12N15/00, C12N5/00	FEATURES	Query Match
CC		source	Score 33.6; DB 6; Length 127;
FT	Key	FT	Best Local Similarity 81.2%; Pred. No. 0.097;
FT	source	source	0; Mismatches 9; Indels 0; Gaps 0;
			;/organism="Nicotiana tabacum" /mol_type="genomic DNA" /db_xref="#taxon:4097"
ORIGIN		FEATURES	Best Local Similarity 81.2%; Pred. No. 0.097;
		source	0; Mismatches 9; Indels 0; Gaps 0;
Query Match		ORIGIN	
Best Local Similarity 81.2%; Pred. No. 0.097;		FEATURES	Query Match
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;		source	Score 33.6; DB 6; Length 127;
Qy	16 GTGGGATTCAGCTGAGGGGCTCCCTAGGCTATTAGGAGCCGAA 63	FT	Best Local Similarity 81.2%; Pred. No. 0.097;
Db	53 GTGGGATTCAGCTGAGGGGCTCCCTAGGCTATTAGGAGCCGAA 100	source	0; Mismatches 9; Indels 0; Gaps 0;
RESULT 7		ORIGIN	
LOCUS	AR399398	FEATURES	Query Match
DEFINITION	Sequence 16 from patent US 66260601.	source	Score 33.6; DB 6; Length 127;
ACCESSION	AR399398	FT	Best Local Similarity 81.2%; Pred. No. 0.097;
VERSION	AR399398.1	source	0; Mismatches 9; Indels 0; Gaps 0;
KEYWORDS	GI: 40141264	ORIGIN	
ORGANISM	Unknown.	FEATURES	Query Match
	Unknown.	source	Score 33.6; DB 6; Length 127;
REFERENCE	1 (bases 1 to 127)	FT	Best Local Similarity 81.2%; Pred. No. 0.097;
AUTHORS	Yamaguchi, I., Nakashita, H., Yoshioka, K. and Doi, Y.	source	0; Mismatches 9; Indels 0; Gaps 0;
TITLE	Methods for transformation of plants, transformed plants and processes for preparation of polyesters	ORIGIN	
JOURNAL	Patent: US 66260601-A 16 16-SEP-2003; Riken, Saitama; JPK;	FEATURES	Query Match
		source	Score 33.6; DB 6; Length 127;
Query Match		FT	Best Local Similarity 81.2%; Pred. No. 0.097;
Best Local Similarity 81.2%; Pred. No. 0.097;		source	0; Mismatches 9; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;		ORIGIN	
Qy	16 GTGGGATTCAGCTGAGGGGCTCCCTAGGCTATTAGGAGCCGAA 63	FEATURES	Query Match
Db	53 GTGGGATTCAGCTGAGGGGCTCCCTAGGCTATTAGGAGCCGAA 100	source	Score 33.6; DB 6; Length 127;
RESULT 8		FT	Best Local Similarity 81.2%; Pred. No. 0.097;
LOCUS	AX137514	source	0; Mismatches 9; Indels 0; Gaps 0;
		ORIGIN	
Query Match		FEATURES	Query Match
Best Local Similarity 81.2%; Pred. No. 0.097;		source	Score 33.6; DB 6; Length 142;
Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;		FT	Best Local Similarity 81.2%; Pred. No. 0.097;
Qy	16 GTGGGATTCAGCTGAGGGGCTCCCTAGGCTATTAGGAGCCGAA 63	source	0; Mismatches 9; Indels 0; Gaps 0;
Db	53 GTGGGATTCAGCTGAGGGGCTCCCTAGGCTATTAGGAGCCGAA 100	ORIGIN	

RESULT 10	AX076661	AX076661 Sequence 1 from Patent WO0101331.	168 bp	DNA	linear	PAT 06-FEB-2001	KEYWORDS ORGANISM	Unknown. Unknown.
DEFINITION	Sequence 1 from Patent WO0101331.						REFERENCE AUTHORS	1 (bases 1 to 184) Bogosian,G., O'Neil,J.P. and Staub,J.M.
ACCESSION	AX076661						TITLE	Bacterial expression systems based on plastidic or mitochondrial
VERSION	AX076661.1	GI:12711193					DEFINITION	Promoter combinations
KEYWORDS	unidentified						ACCESSION	Patent: US 6218145-A 3 17-APR-2001;
SOURCE	unidentified						VERSION	Location/Qualifiers
ORGANISM	unclassified						KEYWORDS	1..184 /organism="unknown" /mol_type="unassigned DNA"
REFERENCE	1.						FEATURES	
AUTHORS	Staub,J.M.						ORIGIN	
TITLE	Enhanced expression of proteins using GFP						Query Match	53.3%; Score 33.6; DB 6; Length 184;
JOURNAL	Patent: WO 0101331-A 1 18-JAN-2001;						Best Local Similarity	81.2%; Pred. No. 0.096; 0; Gaps
FEATURES	Calgene LLC (US)						Matches	0; Mismatches 9; Indels 0; Gaps 0;
SOURCE	Location/Qualifiers						Qy	16 GTGGGATTCACGTTAGGGGGCTCCCTAGGCTATATTAGGGAGCGAA 63
	1..168						Db	42 GTGGGATTCACGTTAGGGGGCTCCCTAGGCTATATTCTGGAGCGAA 89
ORIGIN	/organism="unidentified" /mol_type="unassigned DNA" /db_xref="taxon:32644"							
RESULT 11	CQ797808	CQ797808 Sequence 14 from Patent WO2004029256.	176 bp	DNA	linear	PAT 20-APR-2004	KEYWORDS ORGANISM	Unknown. Unknown.
DEFINITION	Sequence 14 from Patent WO2004029256.						REFERENCE AUTHORS	1 (bases 1 to 201) Malica,P., Allison,L.A. and Hajdukiwicz,P.T.
ACCESSION	CQ797808						TITLE	Nuclear encoded transcription system in plastids of higher plants
VERSION	CQ797808.1	GI:16426081					DEFINITION	Patent: US 6472586-A 29-OCT-2002;
KEYWORDS	synthetic construct						ACCESSION	Rutgers, The State University of New Jersey; Piscataway, NJ
SOURCE	synthetic construct						VERSION	1..201 /organism="unknown" /mol_type="genomic DNA"
ORGANISM	other sequences; artificial sequences.						FEATURES	
REFERENCE	1.						ORIGIN	
AUTHORS	selman-housein Sosa,G., aguilar Cabeza,E., gonz lez Quintero,A.D. and ramos gonz lez,O.						Query Match	53.3%; Score 33.6; DB 6; Length 201;
TITLE	Vector for the production of transplastomic angiosperm plants						Best Local Similarity	81.2%; Pred. No. 0.096; 0; Gaps 0;
JOURNAL	Patent: WO 2004029256-A 14 08-APR-2004;						Matches	Mismatches 9; Indels 0; Gaps 0;
FEATURES	CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CUI)						Qy	16 GTGGGATTCACGTTAGGGGGCTCCCTAGGCTATATTAGGGAGCGAA 63
SOURCE	Location/Qualifiers						Db	45 GTGGGATTCACGTTAGGGGGCTCCCTAGGCTATATTCTGGAGCGAA 92
	1..176							
ORIGIN	/organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630"							
RESULT 12	AR145914	AR145914 Sequence 3 from patent US 6218145.	184 bp	DNA	linear	PAT 08-AUG-2001	KEYWORDS ORGANISM	Unknown. Unknown.
DEFINITION	Sequence 3 from patent US 6218145.						REFERENCE AUTHORS	1 (bases 1 to 202)
ACCESSION	AR145914	GI:15109103					TITLE	Staub,J.M., Ye,G. and Broyles,D.L.
VERSION							DEFINITION	Method for the transformation of plant cell plastids
							ACCESSION	Patent: US 6780033-A 1 24-AUG-2004
							VERSION	Monsanto Technology LLC; St. Louis, MO;
							FEATURES	WOX; Location/Qualifiers 1..202 /organism="unknown"

/mol_type="genomic DNA"

ORIGIN
 Query Match 53.3%; Score 33.6; DB 6; Length 202;
 Best Local Similarity 81.2%; Pred. No. 0.096;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 16 GTGGGATTGACCTGAGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63
 Db 45 GTGGGATTGACCTGAGGGCAAGGGATGGCTATATTCTGGAGCGAA 92

RESULT 15

AX076662
 LOCUS AX076662 Sequence 2 From Patent WO0104331. 202 bp DNA linear PAT 06-FEB-2001
 DEFINITION AX076662
 ACCESSION AX076662.1 GI:12711194
 VERSION
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Staub, J. M.
 TITLE Enhanced expression of proteins using gfp
 JOURNAL Patent: WO 0104331-A 2 18-JAN-2001;
 FEATURES Calgene LLC (US)
 source Location/Qualifiers 1. .202
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32530"
 ORIGIN

Query Match 53.3%; Score 33.6; DB 6; Length 202;
 Best Local Similarity 81.2%; Pred. No. 0.096;
 Matches 39; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 16 GTGGGATTGACCTGAGGGCTCCCTAGGCTATATTAGAGGGAGCGAA 63
 Db 45 GTGGGATTGACCTGAGGGCAAGGGATGGCTATATTCTGGAGCGAA 92

Search completed: February 21, 2006, 06:13:36

Job time : 2171 secs